

β-AMINO ACIDS

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CROSS-REFERENCE TO RELATED APPLICATIONS

This is a continuation-in-part of, and priority is hereby claimed to, co-pending application Serial No. 09/464,212, filed 15 December 1999, which is a divisional of Serial No. 09/034,509, filed March 4, 1998 (now U.S. Patent No. 6,060,585, issued May 9, 2000), which claims priority to provisional patent application Serial Number 60/039,905, filed March 4, 1997, the entire contents of all of which is incorporated herein.

FIELD OF THE INVENTION

The present invention is directed to β-polypeptide molecules which are oligomers and polymers of β-amino acids having stable and well-defined secondary structures, including helices and sheets, methods of generating combinatorial libraries using these β-polypeptides, and combinatorial libraries formed thereby.

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DESCRIPTION OF THE PRIOR ART

Chemists have long sought to extrapolate the power of biological catalysis and recognition to synthetic systems. These efforts have focused largely on low molecular weight catalysts and receptors. Most biological systems, however, rely almost exclusively on large polymers such as proteins and RNA to perform complex chemical functions.

Proteins and RNA are unique in their ability to adopt compact, well-ordered conformations. These two biopolymers are unique also because they can perform complex chemical operations (*e.g.*, catalysis, highly selective recognition, etc.). Folding is linked to function in both proteins and RNA because the creation of an "active site" requires proper positioning of reactive groups. Consequently, there has been a long-felt need to identify synthetic polymer backbones which display discrete and predictable folding propensities (hereinafter referred to as "foldamers") to mimic natural biological systems. Such backbones will provide molecular "tools" to probe the functionality of large-molecule interactions (*e.g.* protein-protein and protein-RNA interactions).

Much work on β -amino acids and peptides synthesized therefrom has been performed by a group led by Dieter Seebach in Zurich, Switzerland. See, for example, *Seebach et al.* (1996) *Helv. Chim. Acta.* 79:913-941; and *Seebach et al.* (1996) *Helv. Chim. Acta.* 79:2043-2066. In the first of these two papers *Seebach et al.* describe the synthesis and characterization of a β -hexapeptide, namely (H- β -HVal- β -HAla- β -HLeu)₂-OH. Interestingly, this paper specifically notes that prior art reports on the structure of β -peptides have been contradictory and "partially controversial." In the second paper, *Seebach et al.* explore the secondary structure of the above-noted β -hexapeptide and the effects of residue variation on the secondary structure.

Dado and Gellman (1994) *J. Am. Chem. Soc.* 116:1054-1062 describe intramolecular hydrogen bonding in derivatives of β -alanine and γ -amino butyric acid. This paper postulates that β -peptides will fold in manners similar to α -amino acid polymers if intramolecular hydrogen bonding between nearest neighbor amide groups on the polymer backbone is not favored.

Suhara et al. (1996) *Tetrahedron Lett.* 37(10):1575-1578 report a polysaccharide analog of a β -peptide in which D-glycocylamine derivatives are linked to each other via a C-1 β -carboxylate and a C-2 α -amino group. This class of compounds has been given the trivial name "carbopeptoids."

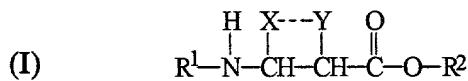
Regarding methods to generate combinatorial libraries, several recent reviews are available. See, for instance, Ellman (1996) *Acc. Chem. Res.* 29:132-143 and Lam et al. (1997) *Chem. Rev.* 97:411-448.

SUMMARY OF THE INVENTION

The present invention is drawn to a genus of conformationally-restricted β -amino acids and β -polyamides which strongly favor a helical or sheet secondary structure and which can serve as building blocks for stable tertiary structures. These stable secondary structures include helices analogous to the well-known α -helical structure seen in α -amino acids. Several of the subject compounds assume helical secondary structures stabilized by hydrogen bonding every 12th or 14th atom of the backbone (12-helix and 14-helix, respectively). Still other compounds according to the invention contain a "reverse turn" residue which mimics the reverse turn often seen in anti-parallel sheet structure seen in conventional peptides and proteins. These β -peptides according to the invention exhibit an anti-parallel secondary sheet structure.

The invention is also directed to the conformationally-restricted β -amino acid monomers. Here, the invention is directed to β -amino acids selected from the group consisting of compounds of Formula I:

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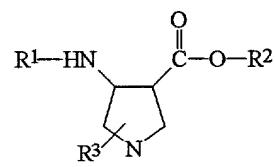
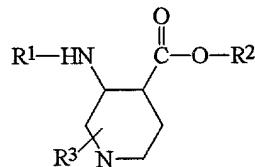
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wherein X and Y combined, together with the carbon atoms to which they are bonded, define a substituted or unsubstituted C_4-C_8 cycloalkyl, cycloalkenyl or heterocyclic ring having one or more nitrogen atoms as the sole heteroatom; the substituents on carbon atoms of the rings being independently selected from the group consisting of linear or branched C_1-C_6 -alkyl, alkenyl, or alkynyl; mono- or bicyclic aryl, mono- or bicyclic heteroaryl having up to 5 heteroatoms selected from N, O, and S; mono- or bicyclic aryl- C_1-C_6 -alkyl, mono- or bicyclic heteroaryl- C_1-C_6 -alkyl, -(CH_2)_{n+1}-OR⁴, -(CH_2)_{n+1}-SR⁴, -(CH_2)_{n+1}-S(=O)-CH₂-R⁴, -(CH_2)_{n+1}-S(=O)₂-CH₂-R⁴, -(CH_2)_{n+1}-NR⁴R⁴, -(CH_2)_{n+1}-NHC(=O)R⁴, -(CH_2)_{n+1}-NHS(=O)₂-CH₂-R⁴, -(CH_2)_{n+1}-O-(CH_2)_m-R⁵, -(CH_2)_{n+1}-S-(CH_2)_m-R⁵, -(CH_2)_{n+1}-S(=O)-(CH₂)_m-R⁵, -(CH₂)_{n+1}-S(=O)₂-(CH₂)_m-R⁵, -(CH₂)_{n+1}-NH-(CH₂)_m-R⁵, -(CH₂)_{n+1}-N-{(CH₂)_m-R⁵}₂, -(CH₂)_{n+1}-NHC(=O)-(CH₂)_{n+1}-R⁵, and -(CH₂)_{n+1}-NHS(=O)₂-(CH₂)_m-R⁵; wherein R⁴ is independently selected from the group consisting of hydrogen, C_1-C_6 -alkyl, alkenyl, or alkynyl; mono- or bicyclic aryl, mono- or bicyclic heteroaryl having up to 5 heteroatoms selected from N, O, and S; mono- or bicyclic aryl- C_1-C_6 -alkyl, mono- or bicyclic heteroaryl- C_1-C_6 -alkyl; and wherein R⁵ is selected from the group consisting of hydroxy, C_1-C_6 -alkyloxy, aryloxy, heteroaryloxy, thio, C_1-C_6 -alkylthio, C_1-C_6 -alkylsulfinyl, C_1-C_6 -alkylsulfonyl, arylthio, arylsulfinyl, arylsulfonyl, heteroarylthio, heteroarylsulfinyl, heteroarylsulfonyl, amino, mono- or di- C_1-C_6 -alkylamino, mono- or diarylamino, mono- or diheteroaryl-amino, N-alkyl-N-arylamino, N-alkyl-N-heteroaryl-amino, N-aryl-N-heteroaryl-amino,

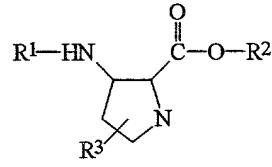
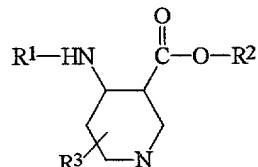
aryl-C₁-C₆-alkylamino, carboxylic acid, carboxamide, mono- or di-C₁-C₆-alkylcarboxamide, mono- or diarylcarboxamide, mono- or diheteroarylcarboxamide, N-alkyl-N-arylcarboxamide, N-alkyl-N-heteroarylcarboxamide, N-aryl-N-heteroarylcarboxamide, sulfonic acid, sulfonamide, mono- or di-C₁-C₆-alkylsulfonamide, mono- or diarylsulfonamide, mono- or diheteroarylsulfonamide, N-alkyl-N-arylsulfonamide, N-alkyl-N-heteroarylsulfonamide, urea; mono- di- or tri-substituted urea, wherein the substituent(s) is selected from the group consisting of C₁-C₆-alkyl, aryl, heteroaryl; O-alkylurethane, O-arylurethane, and O-heteroarylurethane; and m is an integer of from 2-6 and n is an integer of from 0-6; the substituents on heteroatoms of the ring being independently selected from the group consisting of -S(=O)₂-CH₂-R⁴-C(=O)-R⁴-S(=O)₂-(CH₂)_m-R⁵, and -C(=O)-(CH₂)_{n+1}-R⁵; wherein R⁴ and R⁵ are as defined hereinabove, and m is an integer of from 2-6 and n is an integer of from 0-6; provided that when X & Y together with the carbons to which they are bonded define a five- or six-membered cycloalkyl or a five-membered heterocyclic ring having one nitrogen as the sole heteroatom, and the nitrogen is bonded to a carbon atom adjacent to the carboxy carbon of Formula I, the cycloalkyl or heterocyclic ring is substituted; R¹ is selected from the group consisting hydrogen and an amino protecting group; R² is selected from the group consisting of hydrogen and a carboxy protecting group; racemic mixtures thereof, isolated or enriched enantiomers thereof; isolated or enriched diastereomers thereof; and salts thereof.

The preferred embodiment of the invention is a β-amino acid selected from the group consisting of:

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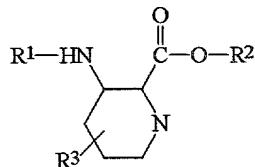


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and

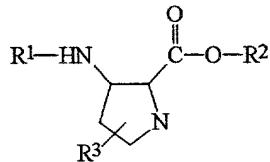


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wherein R^1 is selected from the group consisting hydrogen and an amino protecting group; R^2 is selected from the group consisting of hydrogen and a carboxy protecting group; and when R^3 is bonded to a carbon atom, R^3 is selected from the group consisting of hydrogen, hydroxy, linear or branched C_1-C_6 -alkyl, alkenyl, or alkynyl; mono- or bicyclic aryl, mono- or bicyclic heteroaryl having up to 5 heteroatoms selected from N, O, and S; mono- or bicyclic aryl- C_1-C_6 -alkyl, mono- or bicyclic heteroaryl- C_1-C_6 -alkyl, $-(CH_2)_{n+1}-OR^4$, $-(CH_2)_{n+1}-SR^4$, $-(CH_2)_{n+1}-S(=O)-CH_2-R^4$, $-(CH_2)_{n+1}-S(=O)_2-CH_2-R^4$, $-(CH_2)_{n+1}-NR^4R^4$, $-(CH_2)_{n+1}-NHC(=O)R^4$, $-(CH_2)_{n+1}-NHS(=O)_2-CH_2-R^4$, $-(CH_2)_{n+1}-O-(CH_2)_m-R^5$, $-(CH_2)_{n+1}-S-(CH_2)_m-R^5$, $-(CH_2)_{n+1}-S(=O)-(CH_2)_m-R^5$, $-(CH_2)_{n+1}-S(=O)_2-(CH_2)_m-R^5$, $-(CH_2)_{n+1}-NH-(CH_2)_m-R^5$, $-(CH_2)_{n+1}-N-\{(CH_2)_m-R^5\}_2$, $-(CH_2)_{n+1}-NHC(=O)-(CH_2)_{n+1}-R^5$, and $-(CH_2)_{n+1}-NHS(=O)_2-(CH_2)_m-R^5$; wherein R^4

is independently selected from the group consisting of hydrogen, C₁-C₆-alkyl, alkenyl, or alkynyl; mono- or bicyclic aryl, mono- or bicyclic heteraryl having up to 5 heteroatoms selected from N, O, and S; mono- or bicyclic aryl-C₁-C₆-alkyl, mono- or bicyclic heteroaryl-C₁-C₆-alkyl; and wherein R⁵ is selected from the group consisting of hydroxy, C₁-C₆-alkyloxy, aryloxy, heteroaryloxy, thio, C₁-C₆-alkylthio, C₁-C₆-alkylsulfinyl, C₁-C₆-alkylsulfonyl, arylthio, arylsulfinyl, arylsulfonyl, heteroarylthio, heteroarylsulfinyl, heteroarylsulfonyl, amino, mono- or di-C₁-C₆-alkylamino, mono- or diarylamino, mono- or diheteroaryl amino, N-alkyl-N-arylamino, N-alkyl-N-heteroarylamino, N-aryl-N-heteroarylamino, aryl-C₁-C₆-alkylamino, carboxylic acid, carboxamide, mono- or di-C₁-C₆-alkylcarboxamide, mono- or diarylcarboxamide, mono- or diheteroarylcarboxamide, N-alkyl-N-arylcarboxamide, N-alkyl-N-heteroarylcarboxamide, N-aryl-N-heteroarylcarboxamide, sulfonic acid, sulfonamide, mono- or di-C₁-C₆-alkylsulfonamide, mono- or diarylsulfonamide, mono- or diheteroarylsulfonamide, N-alkyl-N-arylsulfonamide, N-alkyl-N-heteroarylsulfonamide, urea; mono- di- or tri-substituted urea, wherein the substituent(s) is selected from the group consisting of C₁-C₆-alkyl, aryl, heteroaryl; O-alkylurethane, O-arylurethane, and O-heteroarylurethane; and m is an integer of from 2-6 and n is an integer of from 0-6; and when R³ is bonded to a nitrogen atom, R³ is independently selected from the group consisting of those listed above for when R³ is attached to a carbon atom, and further selected from the group consisting of -S(=O)₂-CH₂-R⁴, -C(=O)-R⁴-S(=O)₂-(CH₂)_m-R⁵, and -C(=O)-(CH₂)_{n+1}-R⁵; wherein R⁴ and R⁵ are as defined hereinabove, and m is an integer of from 2-6 and n is an integer of from 0-6; provided that when the β-amino acid is of formula



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R³ is not hydrogen; racemic mixtures thereof, isolated or enriched enantiomers thereof; isolated or enriched diastereomers thereof; and salts thereof.

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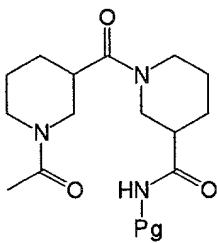
The invention is further directed to a method for preparing a combinatorial library of β-polypeptides, the method comprising at least two successive iterations of first covalently linking a first subunit via its C terminus to a plurality of separable solid substrates, the first subunit being an N-terminus-protected derivative of one of the conformationally-constrained β-amino acids recited hereinabove.

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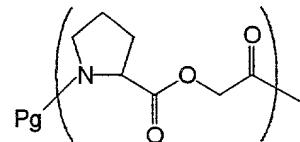
Then randomly dividing the plurality of substrates into at least two sub-groups and deprotecting the N-termini first subunits attached to the at least two sub-groups. Then, in separate and independent reactions, covalently linking to the first subunit of each of the at least two sub-groups a second subunit independently selected from the above-listed group, and, in addition thereto, a residue selected from the group consisting of:

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and



wherein "Pg" is a protecting group. Then combining the at least two subgroups into a single plurality. The process is then repeated one or more times (preferably 5 to 25 times), whereby a combinatorial library of β -amino acid polypeptides is assembled. The invention is further drawn to the
5 combinatorial library of β -polypeptides so formed.

Another embodiment of the invention is drawn to an array comprising a plurality of β -polypeptides as described above at selected, known locations on a substrate or in discrete solutions, wherein each of the polypeptides is substantially pure within each of the selected known locations and has a composition which is different from other polypeptides disposed at other selected and known locations on the substrate.
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The primary advantage of the present invention is that it allows the construction of synthetic peptides of known secondary structures having high conformational stability. These synthetic polyamides have utility in investigating the biological interactions involving biopolymers. The switch in helical hydrogen bond directionality between the β -peptide 12- and 14-helices (See Figs. 2A and 2B) is unprecedented among α -peptides. The residue-based conformational control offered by β -peptides, which was predicted computationally, makes this class of unnatural foldamers well suited for molecular design efforts, *e.g.*, generation of novel tertiary structures, and combinatorial searches for selective biopolymer ligands.
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The β -amino acid monomers are useful for constructing combinatorial libraries of compounds that display peptide behavior (because they are peptides), but resistant to enzymatic degradation because the
25 compounds do not contain any α -peptide linkages.

As a natural consequence, the invention is further drawn to the use of these synthetic β -amino acids as base molecules from which to synthesize large libraries of novel compounds utilizing the techniques of combinatorial chemistry. In addition to varying the primary sequence of the β -amino acid

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residues, the ring positions of these compounds (and notably the equatorial positions in the cyclohexyl-rigidified β -amino acids) can be substituted with a wide variety of substituents, including hydroxy, linear or branched C₁-C₆-alkyl, C₁-C₆-alkyloxy, amino, mono- or di-C₁-C₆-alkylamino, carboxamido, sulfonamido, urea, cyano, fluoro, thio, C₁-C₆-alkylthio, and the like. The main advantage here is that substituents placed on the backbone rings do not substantially alter the secondary structure of the peptide. Consequently, the subject compounds can be utilized to construct vast libraries having different substituents, but all of which share a stabilized secondary structure in both the solid state and in solution.

Thus, the β -amino acids described herein are also useful for fabricating β -polypeptides to model the behavior of corresponding, naturally-occurring α -polypeptide. Because the β -amino acids described herein are not recognized as targets by enzymes that are specific for naturally-occurring α -polypeptides, they can be used in mechanistic studies as non-enzymatically-degradable models of the corresponding α -polypeptide.

Other aims, objects, and advantages of the invention will appear more fully from a complete reading of the following Detailed Description of the Invention and the attached claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the structure of poly- β -alanine and further depicts the hydrogen bonds that define the six narrowest helices available to poly- β -alanine. Poly- β -alanine is the simplest β -peptide polymer.

Fig. 2A depicts the crystal structure of oligomer of *trans*-ACHC/14-helix. The bottom depiction is the two-dimensional structure, the middle depiction is a view along the axis of the helix, and the top depiction is a view perpendicular to the axis of the helix.

Fig. 2B depicts the crystal structure of oligomer of *trans*-ACPC/12-helix. The views shown are the same as in Fig. 2A.

Fig. 2C depicts the crystal structure of a standard α -helix. The views shown are the same as in Fig. 2A.

Fig. 3 depicts ^1H NMR spectra for a solution containing 2 mM *trans*-ACHC dimer and 2 mM *trans*-ACHC hexamer. The bottom spectrum was obtained in CD_3OH with solvent suppression. The two NH resonances from the dimer are indicated with an asterisk (*). All other spectra were obtained in CD_3OD at the times indicated after dissolution of the sample. Data obtained on a Bruker 300 MHz spectrometer at 20°C.

Fig. 4 is a circular dichroism (CD) plot for *trans*-ACPC hexamer in CH_3OH .

Fig. 5 is a CD plot comparing *trans*-ACPC dimer, trimer, tetramer and hexamer.

Fig. 6 depicts ^1H NMR spectra for a solution containing 2 mM of a hexamer of alternating amino-substituted-*trans*-ACHA and *trans*-ACHA. All spectra were obtained in D_2O , 100 mM deuteroacetate buffer, pD 3.9, at the times indicated after dissolution of the sample. Data obtained on a Bruker 300 MHz spectrometer at 20°C.

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Fig. 7 is a comparison between the k_{obs} for amide proton exchange in a hexamer of alternating amino-substituted-*trans*-ACHA and *trans*-ACHA and a dimer of alternating amino-substituted-*trans*-ACHA and *trans*-ACHA.

Fig. 8 is a comparison between the CD plot of a hexamer of alternating amino-substituted-*trans*-ACHA and *trans*-ACHA in water and the CD plot of a hexamer of *trans*-ACHC in methanol.

Fig. 9 is a comparison of CD data in methanol for a β -peptide tetramer, hexamer, and octamer containing alternating *trans*-ACPA residues and 4-pyrrolidinyl residues.

Fig. 10 is a comparison of CD data in water for a β -peptide tetramer, hexamer, and octamer containing alternating *trans*-ACPA residues and 4-pyrrolidinyl residues.

Fig. 11 is a superimposed plot of the CD data in water and the CD data in methanol for the octamer containing alternating *trans*-ACPA residues and 4-pyrrolidinyl residues.

Fig. 12 is a CD spectrum in water of an octamer containing alternating *trans*-ACPA residues and 3-pyrrolidinyl residues.

Fig. 13 is a comparison of CD spectra for a hexamer containing alternating residues of *trans*-ACHA and amino-substituted-*trans*-ACHA and for a "mixed" β -peptide hexamer comprising alternating residues of *trans*-ACHA and an acyclic β -amino acid bearing an aminopropyl substituent on the β -carbon of the backbone.

Fig. 14A shows the infrared spectrum of two linked nipecotic acid residues wherein the two residues have the same absolute configuration.

Fig. 14B shows the infrared spectrum of two linked nipecotic acid residues wherein the two residues have the opposite absolute configuration. This diastereomer acts as a reverse turn in β -peptides which adopt a sheet structure.

Fig. 15 is a schematic representation of the "split and pool" method of generating combinatorial libraries.

Fig. 16 is a ball and stick representation of the solid state conformation of compound 1 described below. For clarity, all hydrogen atoms, except for those attached to nitrogen, have been omitted. Hydrogen bonds are indicated with dotted lines.

DETAILED DESCRIPTION OF THE INVENTION

The first step in creating a foldamer is to identify polymeric backbones with well-defined secondary structural preferences.

Helices in β -Peptides:

Initial molecular modeling studies indicated that β -amino acid oligomers (" β -peptides") are well suited for adoption of compact secondary structures stabilized by intramolecular hydrogen bonds. Fig. 1 shows the hydrogen bonds that define the six narrowest helices available to poly- β -alanine, the simplest β -peptide polymer. The 12-, 16-, and 20-helices (nomenclature derived from hydrogen-bonded ring size) contain hydrogen bonds from carbonyls toward NH groups in the N-terminal direction, as observed for 3_{10} - and α -helices in proteins, while the 10-, 14-, and 18-helices contain hydrogen bonds from carbonyls to NH groups in the N-terminal direction. Molecular mechanics studies of a β -alanine decamer suggested that all six of these helices constitute local minima on the conformational energy surface. β -Alanine oligomers, however, have been shown experimentally to be unordered in solution and to adopt sheetlike packing patterns in the solid state.

Incorporation of the two backbone carbons of a β -amino acid into a small carbocycle or heterocycle provides substantial rigidity to the

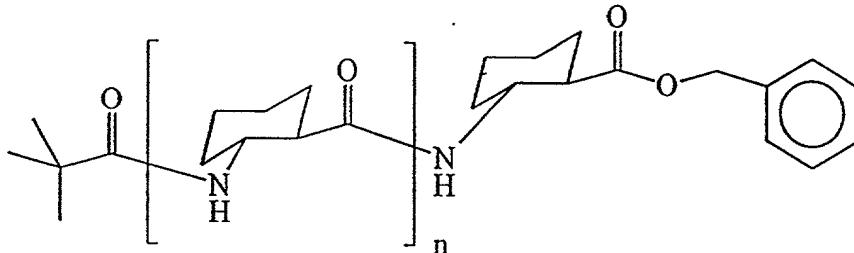
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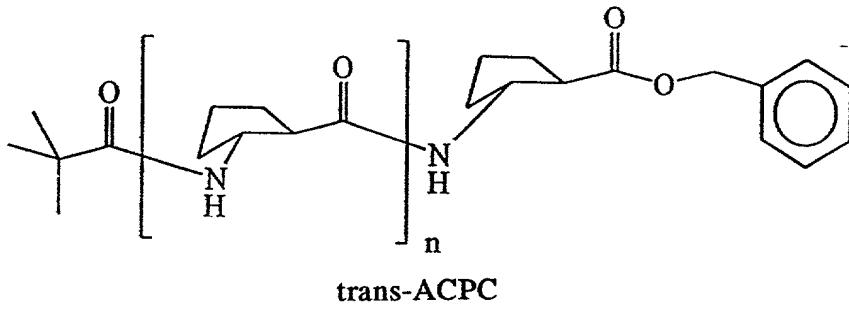
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backbone. Computational methods were used to evaluate whether any particular helix/small ring combination would lead to enhanced conformational stability. For each of the six minimized deca- β -alanine helices shown in Fig. 1, each residue was modified by incorporation of the backbone carbons into a three-, four-, five-, and six-membered cycloalkyl ring. For each ring size, both *cis* and *trans* relationships between the amino and carboxyl substituents were examined, and for the *cis* rings, both of the possible ring orientations relative to the helix were examined. This process yields 72 helical starting structures (6 helices x 4 cycloalkyl ring sizes x (1 *trans* + 2 *cis* forms)). A combination of minimization and dynamics studies predicted that the 14-helical form of the decamer of *trans*-2-aminocyclohexanecarboxylic acid (*trans*-ACHC) (the corresponding monomer is referred to herein as *trans*-ACHA) and the 12-helical form of the decamer of *trans*-2-aminocyclopentanecarboxylic acid (*trans*-ACPC) (corresponding monomer referred to as *trans*-ACPA) would be the most stable among these hypothetical helices. These two structures are shown below:



trans-ACHC

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In order to test this computational prediction, optically active *trans*-AHC was prepared by the reported route, Nohira et al. (1970) *Bull. Chem. Soc. Jpn.* 43:2230, and polypeptide oligomers synthesized via standard methods (see below). The crystal structures of the *trans*-AHC tetramer and the *trans*-AHC hexamer reveal that these molecules adopt 14-helical conformations in the solid state. The hexamer crystal contains three independent but very similar molecules, each of which forms the four possible 14-membered ring hydrogen bonds. The regular helix revealed by the hexamer crystal structure matches the minimum energy conformation predicted for the decamer.

An alternatively rigidified β -amino acid, *trans*-2-aminocyclopentanecarboxylic acid (*trans*-ACPC), provides β -peptides with a dramatically altered secondary structure, the 12-helix. Fig. 2B depicts the 12-helix *trans*-ACPC structure, as compared to a standard α -helix (Fig. 2C) and *trans*-AHC/14-helix (Fig. 2A). This finding shows that β -peptides allow profound residue-based control of peptide conformation.

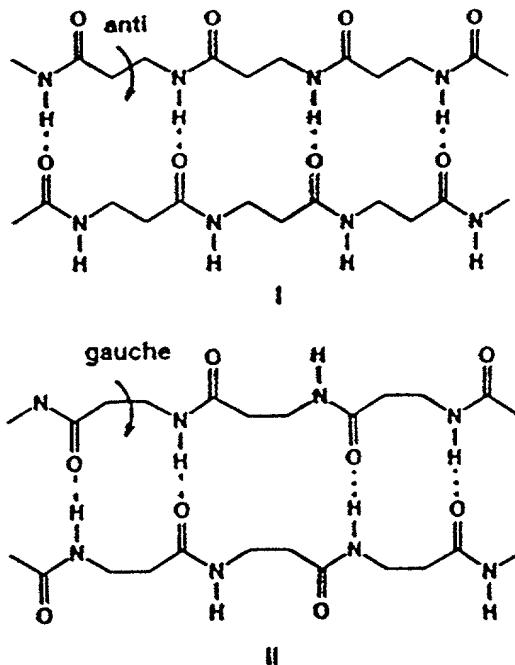
Sheets:

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There are two types of antiparallel β -peptide sheet structures:

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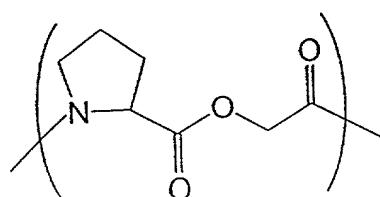
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The type I sheet has a net dipole due to the parallel disposition of the carbonyl groups. In contrast, the type II sheet does not have a net dipole because the carbonyl groups are anti-parallel. This is distinctly different from α -peptides, which can only form sheet structures with anti-parallel carbonyl groups.

Creating discrete model systems of sheet formation using α -amino acids remains a long-standing challenge in protein science. The difficulty lies in designing a moiety to mimic the reverse turn, thereby bringing two attached strands together to form the sheet structure without inducing uncontrolled aggregation of the bulk peptide.

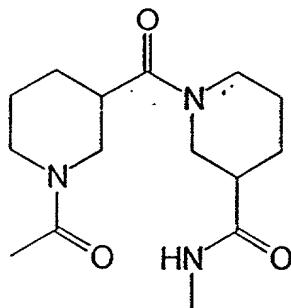
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In the present invention, this problem has been addressed with two moieties which act as the "turn" in the "hairpin" to bring the two peptide chains into alignment to form sheet structures. The first moiety, a prolyl-glycolic acid linkage appears as follows:



The second moiety contains two residues of nipecotic acid:

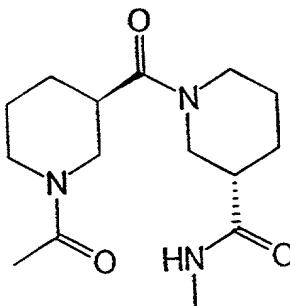
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In the di-nipecotic acid residue it is preferred, although not required, that the two nipecotic acid moieties have opposite absolute configuration:

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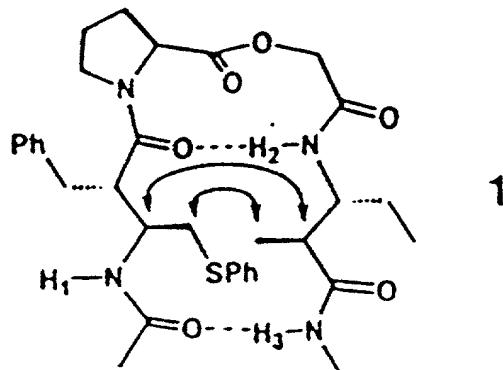
Using these linkages, β -peptide molecules having stable sheet structures were obtained.

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Analysis of solid state and solution phase conformations of the class of molecules described herein were established using a combination of NMR spectroscopy (including COSY, ROESY and NOESY spectra), IR spectrophotometry, circular dichroism, and X-ray crystallography. For compound 1 (described below), NOESY measurements in both CD_2Cl_2 and CD_3OD reveal two long-range NOEs between the β -amino acid residues (curved lines in following structure, both of which are consistent with the solid state conformation depicted in Fig. 16:

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The model compound **1** displays secondary conformation with the two β -amino acid residues intramolecularly arranged in type I antiparallel sheet fashion.

Chemistry:

General. Melting points are uncorrected. CH_2Cl_2 was freshly distilled from CaH_2 under N_2 . DMF was distilled under reduced pressure from ninhydrin and stored over 4 \AA molecular sieves. Triethylamine was distilled from CaH_2 before use. Other solvents and reagents were used as obtained from commercial suppliers. For BOC removal, 4 M HCl in dioxane was used. Column chromatography was carried out by using low air pressure (typically 6 psi) with 230-400 mesh silica gel 60. Routine $^1\text{H-NMR}$ spectra were obtained on a Bruker AC-300 and are referenced to residual protonated NMR solvent. Routine $^{13}\text{C-NMR}$ spectra were obtained on a Bruker AC-300 and are referenced to the NMR solvent. High resolution electron impact mass spectroscopy was performed on a Kratos MS-80RFA spectrometer with DS55/DS90.

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Infrared Spectroscopy. Spectra were obtained on a Nicolet Model 740 FT-IR spectrometer. IR samples were prepared under anhydrous conditions; CH_2Cl_2 was freshly distilled from CaH_2 , compounds and glassware were dried under vacuum for 1-2 days, and solutions were prepared under a nitrogen atmosphere. The pure solvent spectrum for a

particular solution was subtracted from the sample spectrum prior to analysis. Peaks in the amide NH stretch region were baseline corrected, and analyzed without further manipulation.

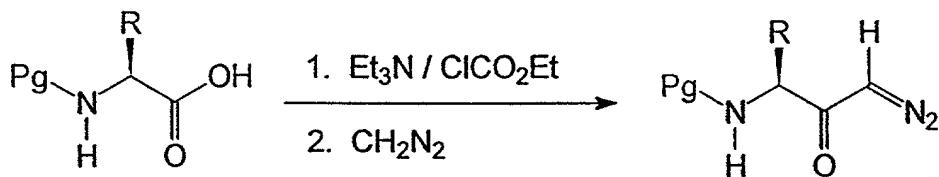
5 **NMR Spectroscopy. 1. Aggregation Studies.** One-dimensional spectra for aggregation studies were obtained on a Bruker AC-300 spectrometer. Samples for aggregation studies were prepared by serial dilution from the most concentrated sample (50 mM or 27 mM). Dry compounds were dissolved in CD₂Cl₂ previously dried over 3 Å molecular sieves, and samples were prepared with dry glassware under a nitrogen atmosphere.

10 **2. Conformational Analysis.** NMR samples for conformational analysis were prepared by dissolving the dry compound in dry deuterated solvent under a nitrogen atmosphere. CD₂Cl₂ samples were then degassed by the freeze-pump-thaw method, and the NMR tubes were sealed under vacuum. Methanol samples were sealed with a close fitting cap and parafilm. COSY spectra were obtained on a Bruker AC-300 spectrometer. TOCSY (Braunschweiler, L.; Ernst, R. R. (1983) *J. Magn. Reson.* 53:521), NOESY (Macura, S.; Ernst, R. R. (1980) *Mol. Phys.* 41:95), and ROESY (Bothner-By, A. A.; Stephens, R. L.; Lee, J.; Warren, C. D.; Jeanloz R. W. (1984) *J. Am. Chem. Soc.* (1984) 106:811) spectra were recorded on a Varian Unity-500 spectrometer using standard Varian pulse sequences and hypercomplex phase cycling (States-Haberkorn method), and the data were processed with Varian "VNMR" version 5.1 software. Proton signals were assigned via COSY and TOCSY spectra, and NOESY and ROESY spectra provided the data used in the conformational analyses. TOCSY spectra were recorded with 2048 points in t₁, 320 or 350 points in t₂, and 8 or 40 scans per t₂ increment. NOESY and ROESY spectra were recorded with a similar number of t₁ and t₂ points, and 32 and 40 scans per t₂ increment, depending on the sample concentration. The width of the spectral window

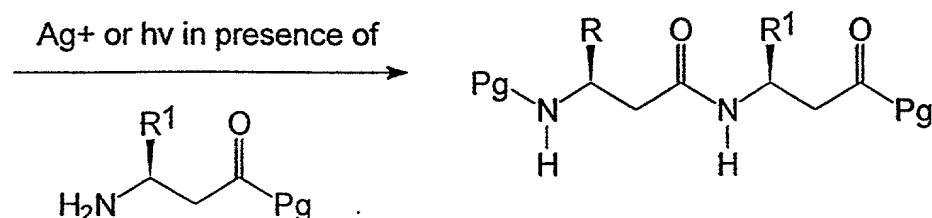
examined was between 2000 and 4000 Hz. Sample concentrations for two-dimensional spectra were 2 mM in CD₂Cl₂ and 8 mM in CD₃OD and CD₃OH.

Far UV Circular Dichroism (CD). Data were obtained on a Jasco J-715 instrument at 20°C. In all CD plots contained herein, the mean residue ellipticity is presented on the vertical axis. Presenting the mean residue ellipticity is a standard practice in peptide chemistry wherein the intensity of each CD spectrum is normalized for the number of amide chromophores in the peptide backbone. Consequently, when the intensities of the maximum (ca. 205 nm) and minimum (ca. 220 nm) peaks characteristic of helix formation increase with increasing chain length, this change represents an increase in the population of the helix structure, rather than simply an increase in the number of chromophores present in each molecule.

Synthesis. The β-amino acids used to assemble the peptides described herein can be manufactured using several different literature methods, as well as new methods described below. For unsubstituted β-amino acids and β-amino acids containing one or two acyclic substituents on the carbon adjacent to the amino group in the product β-peptide, the Arndt-Eisterdt homologation reaction can be used, see Reaction 1. See also Seebach et al. (1996) *Helv. Chim. Acta* 79:913. This route has advantages and disadvantages. A distinct advantage is that the starting materials, α-amino acids, are readily available commercially in enantiomerically pure form. The Arndt-Eisterdt homologation also results in the simultaneous coupling of two β-amino residues. A distinct disadvantage is that the reaction cannot be used to synthesize β-amino acids having rings in the backbone or α-carbon substituents. The reaction proceeds via a Wolff rearrangement of a diazoketone with subsequent trapping of the reactive intermediate with an amino moiety, as shown in Reaction 1:



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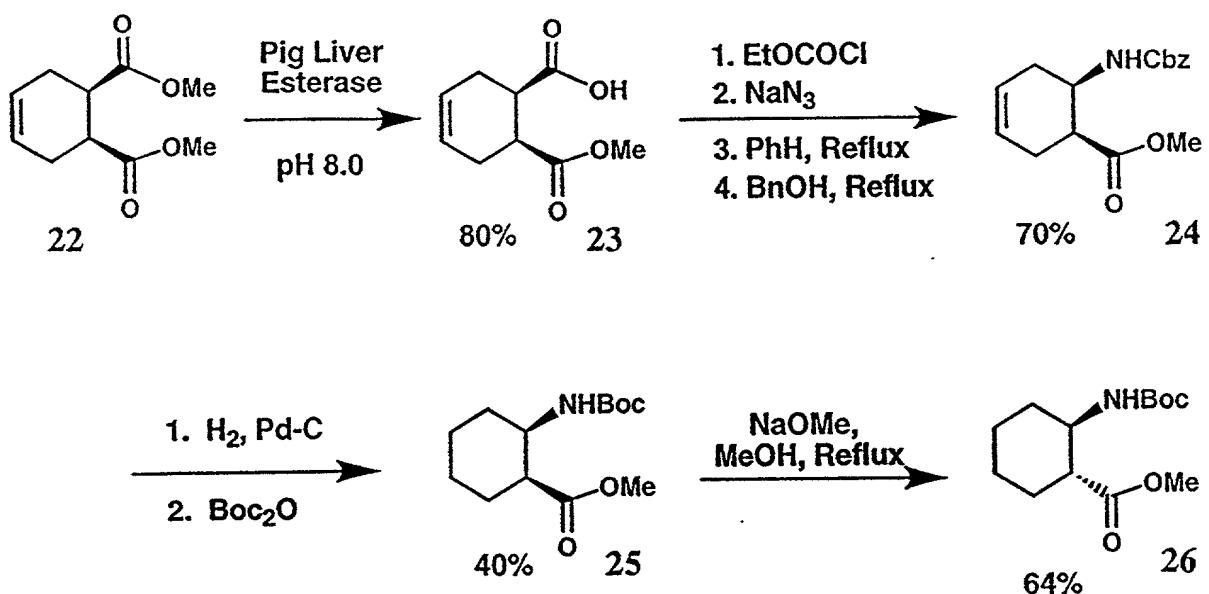


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(Pg designates a protecting group such as (t-butoxy)carbonyl (Boc) or an adjacent β -amino residue, R^1 and R^2 are aliphatic substituents.

β -Amino acids containing an unsubstituted cycloalkyl moiety involving the α and β carbons were synthesized using literature methods. See, for example, Nohira *et al.* (1970) *Bull. Chem. Soc. Jpn.* 43:2230; Herradon and Seebach (1989) *Helv. Chim. Acta* 72:690-714; and Tilley *et al.* (1992) *J. Med. Chem.* 35:3774-3783, all three of which are incorporated herein by reference.

In particular, the cyclohexyl-containing β -amino acids can be synthesized via Reaction 2:



REACTION 2

(1*R*,6*S*)-6-Methoxycarbonyl-3-cyclohexene-1-carboxylic acid (23):

4600 u of PLE was suspended in pH 8.01 aqueous buffer solution (0.17 M KH₂PO₄). The diester **22** (10.1 g, 0.05 mol) was dissolved in 30 mL of acetone and added to the buffer solution. Reaction was allowed to stir at rt overnight. The enzyme was filtered off through a well-packed celite pad, the solution was then acidified to pH 1 with 1M HCl and the product was extracted with ethyl acetate (5 x 400 mL). The combined organic extracts were dried over anhydrous magnesium sulfate and concentrated to yield 9.00 g yellow oil. Product taken on without further purification.

Methyl (1*S*,6*R*)-6-benzyloxycarbonylaminocyclohex-3-ene carboxylate (24): Ethylchloroforamate (4 mL, 0.042 mol) was added to a mixture of **23** (5.14 g, 0.028 mol) and triethylamine (6 mL, 0.043 mol) in acetone (100 mL) at 0° C and vigorously stirred for 10 min. An aqueous solution of NaN₃ (3.04 g, 0.047 mol, in 25 mL water) was added in one portion. The resulting mixture was stirred for 30 min at 0° C. The reaction mixture was diluted with water and extracted with diethyl ether. The organic extracts were dried over anhydrous magnesium sulfate and concentrated without heat to yield a viscous yellow liquid. The liquid was dissolved in 100 mL of benzene and refluxed under nitrogen atmosphere for 30 min. Benzyl alcohol (12 mL, 0.116 mol) was added and solution was refluxed for an additional 16 h. The reaction was cooled to rt and concentrated to yield 17.12 g of a yellow liquid (mixture of benzyl alcohol and desired product in a 5.4:1 ratio, respectively by ¹H NMR, ~5.67 g product). Mixture taken on without further purification.

Methyl (1*S*,6*R*)-6-*tert*-butoxycarbonylaminocyclohexane carboxylate (25): The yellow oil from the previous reaction, which contains compound **24** (5.6 g, 0.020 mol) and benzyl alcohol, was dissolved in methanol. 0.525 g of 10% Pd on carbon was added to the methanol solution, and the heterogenous mixture was placed under 50 psi H₂ and

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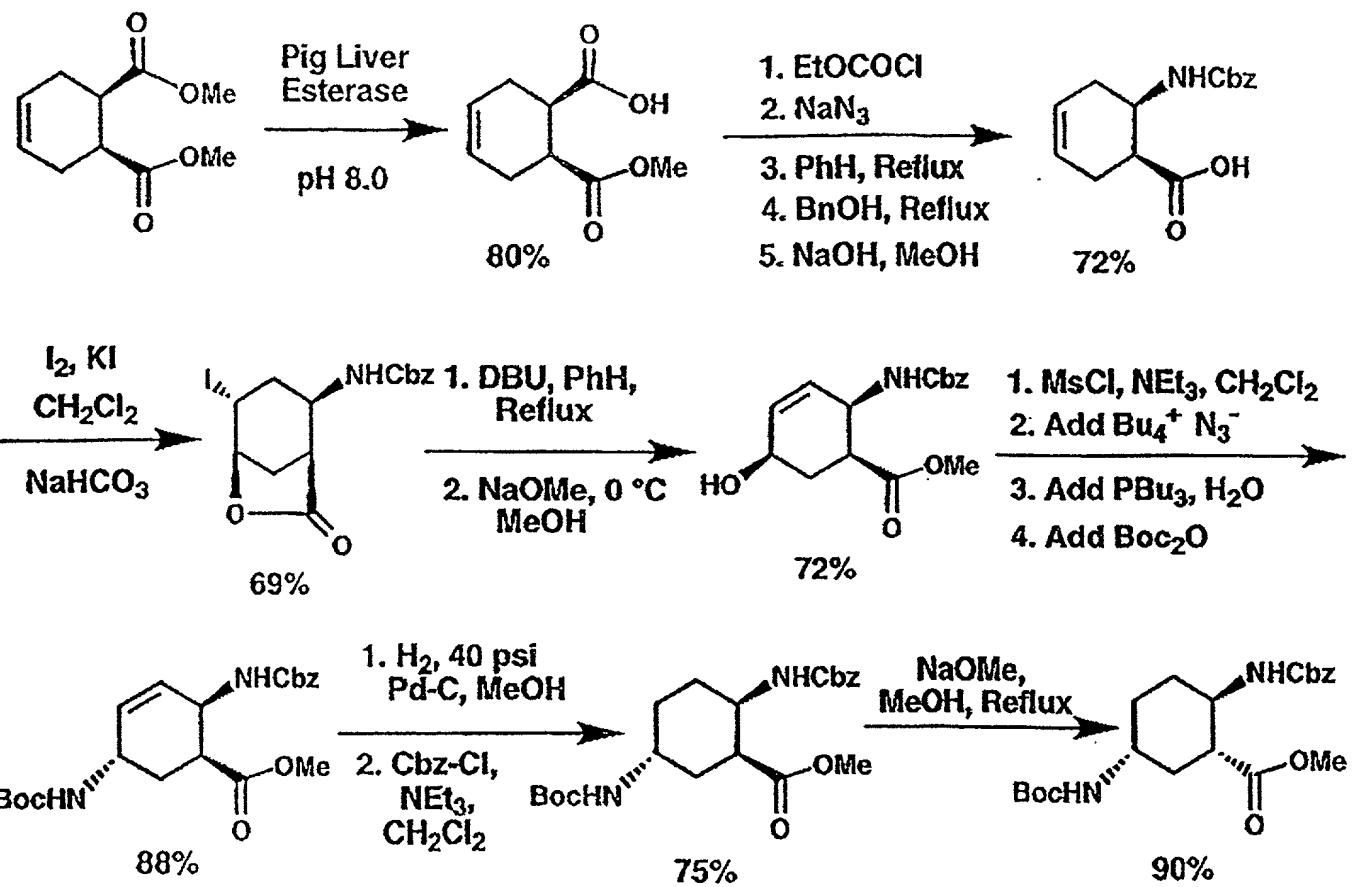
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shaken at rt for 24 h. The mixture was filtered through celite, and the filtrate was concentrated to yield 13.74 g of dark golden yellow liquid. 25 mL of 1M HCl was added to the filtrate, and the benzyl alcohol was extracted with diethyl ether (3 x 25 mL). The pH of the aqueous solution was adjusted to 9 using K₂CO₃. 25 mL of dioxane and Boc₂O (5 g, 0.023 mol) were added to the solution, and the reaction was stirred at rt for 20 h. 15 mL of water was added and the solution was extracted with ethyl acetate (3 x 50 mL). The combined organic extracts were dried over anhydrous magnesium sulfate and concentrated. Residue was purified via column chromatography (SiO₂, eluting with 6:1 Hex:EtOAc), to yield 2.00 g viscous clear oil.

Methyl (IR,6R)-6-tert-butoxycarbonylaminocyclohexane carboxylate (26): Sodium metal (0.14 g, 6.1 mmol) was placed into a flame dried flask under nitrogen atmosphere and cooled to 0° C. 10 mL of freshly distilled methanol was added and the mixture stirred until all the sodium dissolved. An amount of **25** (2.00 g, 7.7 mmol) was dissolved in 10 mL of freshly distilled methanol and transferred to NaOMe solution via cannula. The solution was refluxed under nitrogen for 5.5 h, cooled to rt and acidified with 0.5 M aqueous 0.5 M ammonium chloride (18 mL, 9 mmol). The methanol was removed under reduced pressure, and the resulting solid collected by filtration to yield 1.27 g of desired product.

β-Amino acids containing a substituted cycloalkyl moiety were synthesized using the following illustrative protocol, the first four steps of which are described in Kobayashi *et al.* (1990) *Chem.Pharm.Bull.* (1990) 38:350. The remaining steps to yield a cyclohexyl ring having two differentially protected amino substituents were developed in furtherance of the present invention and have not heretofore been described in the literature and are shown in Reaction 3:



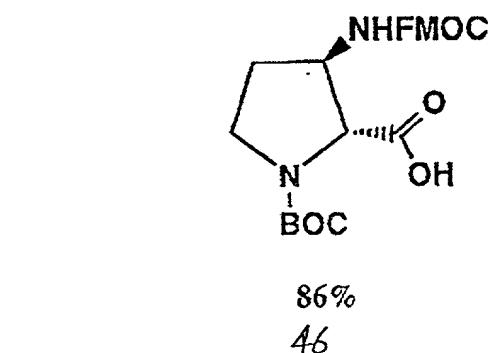
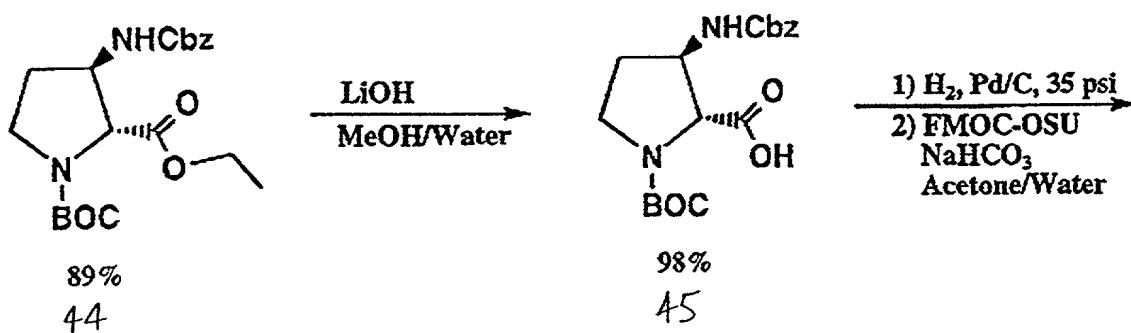
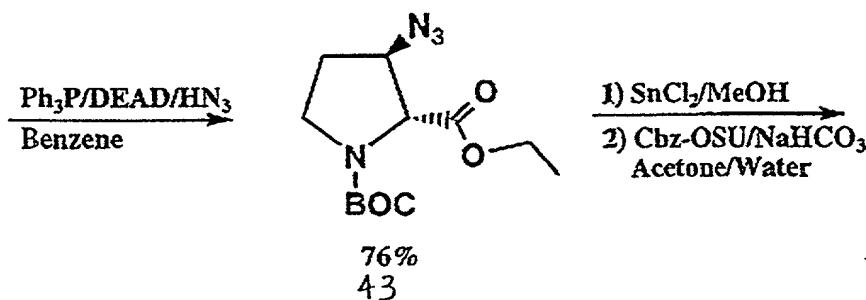
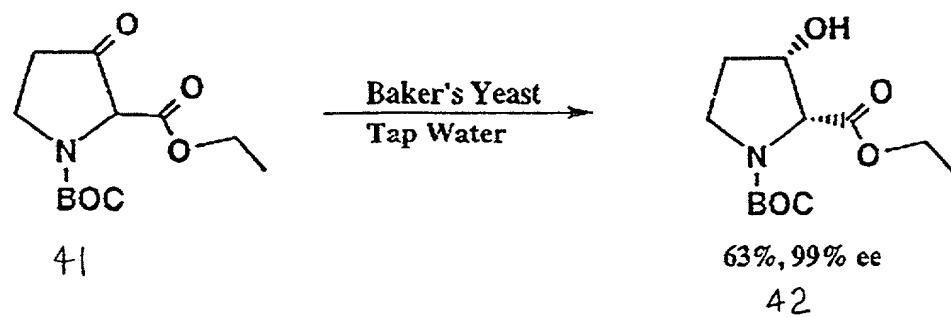
REACTION 3

As depicted in Reaction 3, the 4-position amino substituent is protected by a Boc group and the 1-position amino substituent is protected by a Cbz group. The starting material is available commercially (Aldrich Chemical Co., Milwaukee, Wisconsin).

Synthesis of β -amino acids containing a heterocyclic ring moiety encompassing the α and β carbons were synthesized using Reactions 4 and 5, below. Reaction 4 details an illustrative synthesis of a β -proline wherein the exocyclic amino substituent is in the 3-position relative to the ring nitrogen.

Compound 42: Tap water (200 ml) and baker's yeast (25 g) were mixed, and were shaken on an orbital shaker for 1 hour. Compound 41 (1.0 g) was then added. The mixture was shaken at room temperature for 24 hours. The mixture was filtered through a bed of Celite. The Celite was washed with water (20 ml). The filtrate was extracted with diethyl ether (5 x 100 ml). The extracts were washed with water (2 x 50 ml), dried over $MgSO_4$, and concentrated to yield a slightly yellow oil. The crude product was purified by column chromatography with ethyl acetate/hexane (1/1, v/v) as eluent to give a colorless oil (0.5 g) in 50% yield.

Compound 43: Compound 42 (228 mg) and Ph_3P (346 mg) were dissolved in benzene (anhydrous, 4 ml) under nitrogen. HN_3 (1.64 M in benzene, 0.8 ml) was then added. A solution of diethyl azodicarboxylate (0.18 ml) in benzene (1.0 ml) was subsequently introduced via syringe over 5 minutes. The reaction mixture turned cloudy towards the end of the addition. The reaction mixture was stirred under nitrogen at room temperature for 3.0 hours. The reaction mixture was then taken up in ethyl acetate (50 ml), washed with 1N NaOH (10 ml), saturated $NaHCO_3$ (10 ml), and finally dilute brine (5 ml). The organic was dried over $MgSO_4$, and concentrated to give a slightly yellow oil. The crude oil was purified by



DEAD = Diethyl azodicarboxylate
Cbz-OSU = N-(Benzylloxycarbonyloxy)succinimide
Fmoc-OSU = 9-Fluorenylmethyloxycarbonyl-N-hydroxysuccinimide

Starting material: Blake, J. et al *J. Am. Chem. Soc.* 1964, 86, 5293.
 Yeast reduction: Cooper, J. et al *J. Chem. Soc. Perkin Trans. I* 1993, 1313.

REACTION 4

column chromatography with ethyl acetate/hexane (1/1, v/v) as eluent to afford a colorless oil (190 mg) in 76% yield.

Compound **44**: Compound **43** (1.1 g) was dissolved in methanol (50 ml). SnCl₂ (2.2 g) was then added. The mixture was stirred at room temperature for 30 hours. The methanol was then removed under reduced pressure. The residue was dissolved in methylene chloride (50 ml). The resulting cloudy solution was filtered through Celite. The methylene chloride was then removed under reduced pressure. The residual white solid was dissolved in acetone/water (2/1, v/v, 50 ml). NaHCO₃ (3.3 g) was added, followed by Cbz-OSU (1.16 g). The reaction mixture was stirred at room temperature for 24 hours. Water (50 ml) was added. The acetone was removed under reduced pressure. The aqueous mixture was extracted with ethyl acetate (3 x 100 ml). The extracts were washed with dilute brine (30 ml), dried over MgSO₄, and concentrated to give a colorless oil. The crude product was purified by column chromatography with ethyl acetate/hexane (3/7, v/v) as eluent to give the clean product as a colorless oil (1.35 g) in 89% yield.

Compound **45**: Compound **44** (1.35 g) was dissolved in methanol/water (3/1, v/v, 80 ml), cooled to 0° C. LiOH.H₂O (1.68 g) was added. The mixture was stirred at 0° C for 24 hours, by which time TLC indicated that the hydrolysis was complete. Saturated ammonium hydroxide (20 ml) was added. The methanol was removed under reduced pressure. The aqueous was washed with diethyl ether (50 ml), acidified with 1N HCl to pH 3, extracted with methylene chloride (3 x 150 ml). The extracts were washed with dilute brine (50 ml), dried over MgSO₄, concentrated to give a sticky colorless residue (1.25 g, 99%), which was used directly without further purification.

Compound **46**: Compound **45** (1.25 g) was dissolved in methanol (50 ml) in a hydrogenation flask. 5% Palladium on activated carbon (190 mg)

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was added. The flask was pressurized with hydrogen to 35 psi, rocked at room temperature for 7 hours, by which time TLC indicated that the hydrogenolysis was complete. The Pd/C was removed by filtration. The filtrate was concentrated to give a white solid. The white solid was dissolved in acetone/water (2/1, v/v, 70 ml), cooled to 0° C. NaHCO₃ (1.7 g) was added, followed by FMOC-OSU (1.39 g). The reaction mixture was stirred at room temperature for 16 hours. Water (50 ml) was added. The acetone was removed under reduced pressure. The aqueous was washed with diethyl ether (50 ml), acidified with 1N HCl to pH 3, extracted with methylene chloride (3 x 150 ml). The extracts were washed with dilute brine (50 ml), dried over MgSO₄, concentrated to give a foamy white solid. The crude white solid was purified by column chromatography with methanol/ethyl acetate (3/7, v/v) as eluent to give the clean product as a white solid (1.3 g) in 86% yield.

Reaction 5 illustrates the synthesis of a β-amino acid wherein the exocyclic amino substituent the nitrogen heteroatom is in the 4-position relative to the ring nitrogen.

Compound 52: Compound **51** (2.0 g) and NaBH₃CN (0.54 g) were dissolved in methanol (40 ml), 1N HCl (aqueous) was added dropwise to maintain pH 3-4. After 15-20 minutes, pH change slowed. The mixture was stirred for an additional 1.0 hour, while 1N HCl was added occasionally to keep pH 3-4. Water (100 ml) was added. The mixture was extracted diethyl ether (3 x 150 ml). The extracts were washed with 1N NaHCO₃ (100 ml) and dilute brine (100 ml), dried over MgSO₄, and concentrated to give a colorless oil (1.9 g) in 95 % yield. The product was used directly without further purification.

Compound 53: Compound **52** (1.9 g) and Ph₃P (2.8 g) were dissolved in toluene (anhydrous, 30 ml) under nitrogen. A solution of diethyl azodicarboxylate (1.5 ml) in toluene (10 ml) was subsequently

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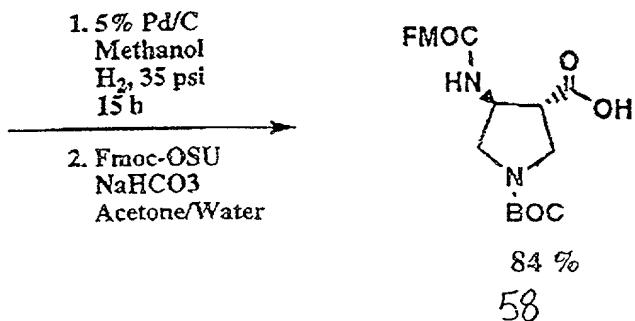
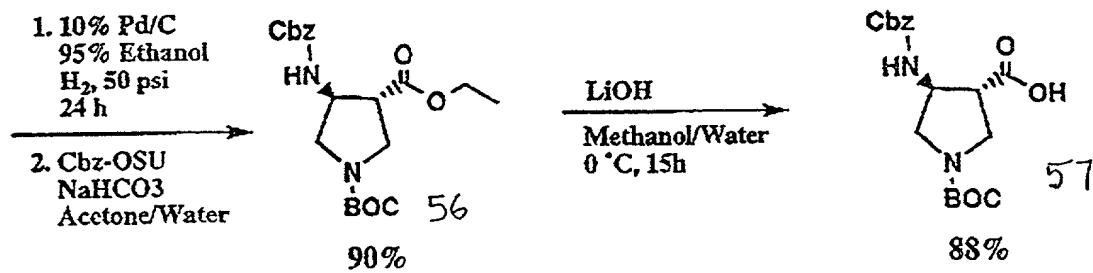
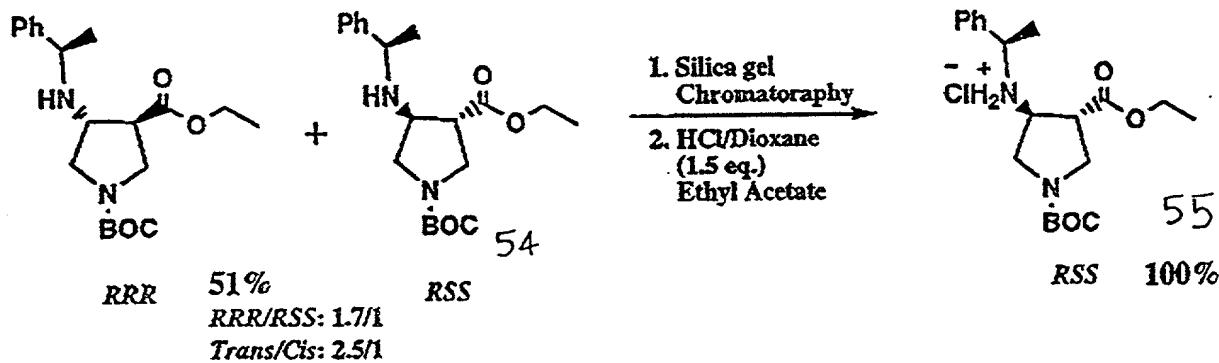
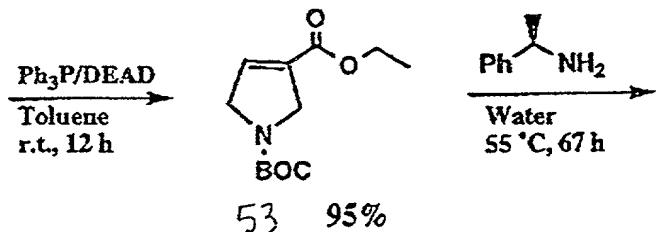
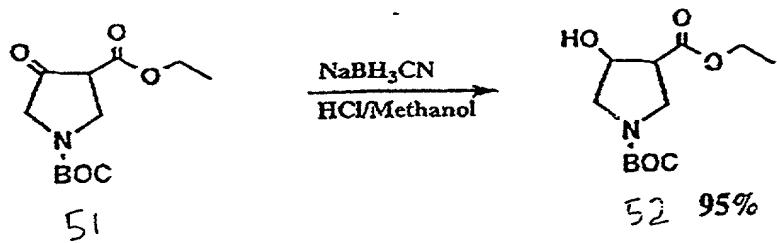
introduced via syringe over 15 minutes. The reaction mixture was stirred under nitrogen at room temperature for 12 hours. The toluene was removed under reduced pressure. The residue was purified by column chromatography with ethyl acetate/hexane (3/7, v/v) as eluent to afford a colorless oil (1.6 g) in 91 % yield.

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Compound 54: Compound 53 (1.0 g) and R-(+)- α -methylbenzylamine (1.1 ml) were mixed with water (15 ml). The mixture was stirred at 55° C for 67 hours. The mixture was taken up in diethyl ether (300 ml), and the aqueous layer was separated. The ether solution was washed with water (3 x 50 ml), dried over MgSO₄, and concentrated to give a slight yellow oil. The diastereometric isomers were separated by column chromatography with ethyl acetate/hexane (2/8, v/v) as eluent to give RSS (0.2 g) and RRR (0.34 g) in 51 % overall yield.

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Compound 55: Compound **54** (4.2 g) was dissolved in ethyl acetate (200 ml). 4N HCl in dioxane (4.35 ml) was added dropwise while stirring. A white precipitate resulted. The ethyl acetate was removed under reduced pressure, and the resulting white solid (4.6 g, 100%) was dried *in vacuo*.



DEAD = Diethyl azodicarboxylate
Cbz-OSU = N-(Benzylloxycarbonyloxy)
 succinimide
Fmoc-OSU = 9-Fluorenylmethyloxycarbonyl-
 N-hydroxysuccinimide

Starting material: Blake, J. et al *J. Am. Chem. Soc.* 1964, 86, 5293.

REACTION 5

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Compound 56: Compound **55** (4.6 g) was dissolved in 95 % ethanol (150 ml) in a hydrogenation flask. 10% Palladium on activated carbon (0.5 g) was added. The flask was pressurized with hydrogen to 50 psi, rocked at room temperature for 22 hours, by which time NMR spectroscopy indicated that the hydrogenolysis was complete. The Pd/C was removed by filtration. The filtrate was concentrated to give a white solid. The white solid was dissolved in acetone/water (2/1, v/v, 150 ml). NaHCO₃ (9.7 g) was added, followed by Cbz-OSU (3.4 g). The reaction mixture was stirred at room temperature for 14 hours. Water (100 ml) was added. The acetone was removed under reduced pressure. The aqueous mixture was extracted with ethyl acetate (3 x 200 ml). The extracts were washed with 1N HCl (3 x 100 ml) and saturated NaHCO₃ (aqueous), dried over MgSO₄, and concentrated to give a colorless oil. The crude product was purified by column chromatography with ethyl acetate/hexane (3/7, v/v) as eluent to give the clean product as a colorless sticky oil (4.0 g) in 90% yield.

Compound 57: Compound **56** (2.0 g) was dissolved in methanol/water (3/1, v/v, 115 ml), cooled to 0° C, LiOH.H2O (2.4 g) was added. The mixture was stirred at 0° C for 15 hours, by which time TLC indicated that the hydrolysis was complete. Saturated ammonium hydroxide (aqueous, 100 ml) was added. The methanol was removed under reduced pressure. The aqueous was acidified with 1N HCl to pH 3, extracted with ethyl acetate (3 x 200 ml). The extracts were washed with dilute brine (100 ml), dried over MgSO₄, concentrated to give a foamy solid (1.63 g, 88%), which was used directly without further purification).

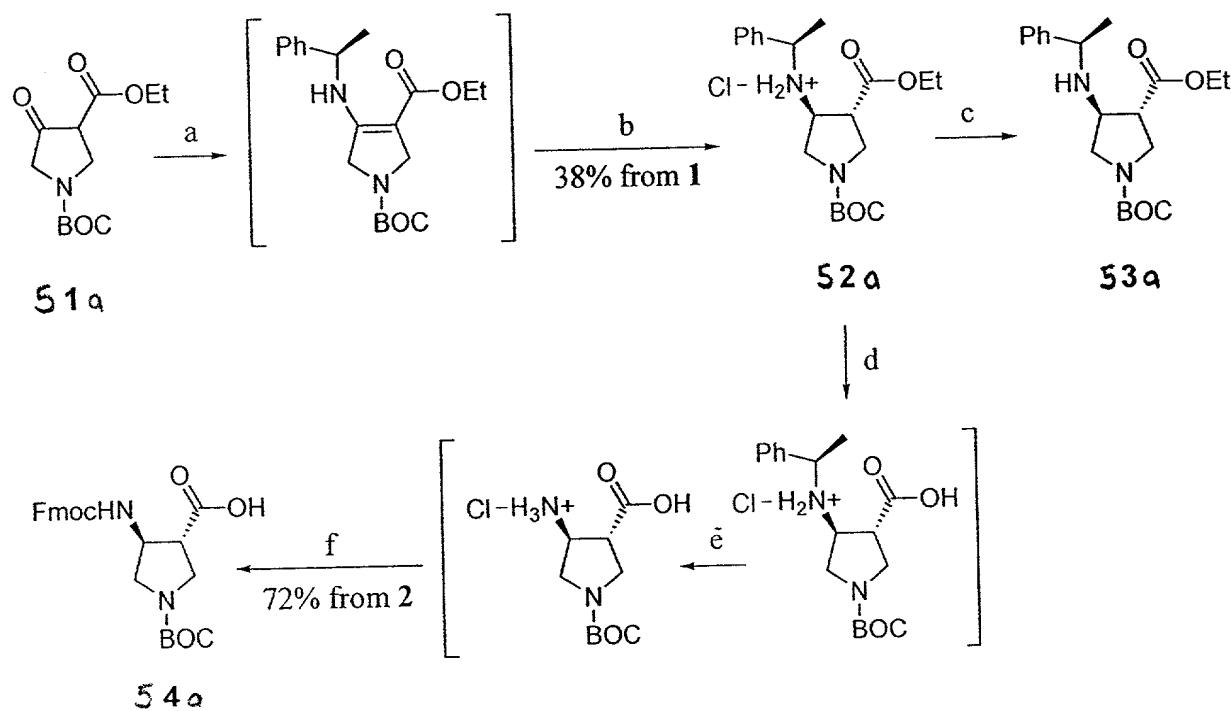
Compound 58: Compound **57** (1.63 g) was dissolved in methanol (70 ml) in a hydrogenation flask. 5% Palladium on activated carbon (250 mg) was added. The flask was pressurized with hydrogen to 35 psi, rocked at room temperature for 15 hours, by which time NMR spectroscopy indicated that the hydrogenolysis was complete. The Pd/C was removed by filtration.

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The filtrate was concentrated to give a white solid. The white solid was dissolved in acetone/water (2/1, v/v, 90 ml), cooled to 0° C. NaHCO₃ (2.27 g) was added, followed by FMOC-OSU (1.83 g). The reaction mixture was stirred at 0° C for 2 hours, then at room temperature for 28 hours. Water (50 ml) was added. The acetone was removed under reduced pressure. The aqueous was acidified with 1N HCl to pH 3, extracted with ethyl acetate (3 x 200 ml). The extracts were washed with dilute brine (100 ml), dried over MgSO₄, concentrated to give a foamy white solid. The crude white solid was purified by column chromatography with methanol/fethyl acetate (3/7, v/v) as eluent to give the clean product as a white solid (1.68 g) in 84% yield.

Reaction 5a illustrates an alternative synthesis of the β-amino acid wherein the exocyclic amino substituent the nitrogen heteroatom is in the 4-position relative to the ring nitrogen. This synthesis is the preferred route.



As compared to Reaction 5, Reaction 5a is streamlined in that the number of chemical operations is reduced and the need for chromatographic separations is eliminated.

Ketoester **51a** is allowed to react with (R)- α -methylbenzylamine in the presence of acetic acid, and the resulting enamine is reduced *in situ* with NaBH₃CN. This reduction produces a mixture of four diastereomeric β -aminoesters in which **52a** is the major product. A two-step crystallization protocol that allows isolation of hydrochloride salt **52a** in diastereomerically pure form. The crude β -aminoester mixture is dissolved in ethyl acetate and converted to a mixture of ammonium salts by treatment with HCl. A single *trans* isomer crystallizes in relatively pure form after this treatment, although there is contamination from the other *trans* isomer. Recrystallization from acetonitrile yields a very pure form of **52a**, in 38% overall yield from **51a**. When (R)- α -methylbenzylamine is used, the purified β -aminoester hydrochloride is spectroscopically identical to material previously identified by crystal structure determination as the diastereomer shown in Reaction 5a. Thus, use of (R)- α -methylbenzylamine leads ultimately to a protected form of (3S,4R)-*trans*-3-aminopyrrolidine-4-carboxylic acid.

The route is completed by alkaline ester hydrolysis, hydrogenolytic removal of the α -methylbenzyl group and Fmoc protection of the resulting amino group. These three steps can be performed in rapid succession, and the final product can be purified by crystallization from n-heptane/ethyl acetate. The protection pattern of diamino acid derivative **54a** is suitable for Fmoc-based synthesis of the β -peptide backbone on a solid support, with deprotection of the pyrrolidine ring nitrogens upon acidolytic cleavage from the resin. The synthetic route outlined in Reaction 5a is amenable to multi-gram synthesis of β -peptide building block **54a** from **51a** in one week.

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Compound **52a**. To a stirred solution of β -ketoester **51a** (16.0 g, 62.3 mmol) in absolute ethanol (250 mL) under N_2 was added (R)-(+)- α -methylbenzylamine (16.0 mL, 124.5 mmol) and glacial acetic acid (7.1 mL, 124.5 mmol) to obtain a cloudy solution. The reaction mixture was stirred at room temperature until the formation of the enamine was complete (3 h, monitored by TLC, product $R_f = 0.55$, 7:3 hexane:ethyl acetate). Sodium cyanoborohydride (16.5 g, 249.2 mmol) was then added to the reaction mixture at room temperature and the resulting solution was heated to 75 °C and stirred for 14 h under N_2 . (This reaction must be carefully monitored by TLC; disappearance of the enamine indicates completion of reaction. Higher temperature and/or longer reaction time leads to formation of an α,β -unsaturated ester side product.) The ethanol was removed via rotary evaporation. Water (250 mL) was added. The mixture was extracted three times with diethyl ether. The combined organic extracts were washed with brine, dried over $MgSO_4$, and concentrated to give a colorless oil. The oil was applied to a plug of silica gel and washed with 2:1 hexane:ethyl acetate. The filtrate was concentrated to obtain a colorless oil. The oil was dissolved in ethyl acetate (250 mL), and 4 N HCl in dioxane (15.6 mL) was added dropwise at room temperature. The resulting solution was cooled to 0 °C and allowed to stand for 3 h at 0 °C. A precipitate formed during this time. The solid was filtered and washed two times with 100 mL portions of ethyl acetate ($\geq 98\% de$, 42% crude yield from **51a**; the diastereomeric excess was determined by GC-MS). This solid could be purified by recrystallization from acetonitrile. The solid was suspended in acetonitrile (200 mL) and heated to reflux for 1 h. The solution was then cooled to 0 °C for 3 h. The resulting solid was filtered and washed two times with 30 mL portions of acetonitrile. The solid was further dried under vacuum to give 9.4 g of **52a** as a white crystalline solid

(>99.0% *de*, 38% yield from **51a**; the diastereomeric excess was determined by GC-MS): mp 190-191 °C, $[\alpha]^{23}_{\text{D}} = 4.8$ (c 1.05, MeOH); ^1H NMR (DMSO-*d*₆, 300 MHz, 24 °C) δ 10.12-9.75 (br, 2H), 7.70-7.28 (m, 5H), 4.54 (m, 1H), 4.05 (q, $J_{\text{HH}} = 7.2$ Hz, 2H), 3.80-3.59 (m, 3H), 3.54-3.22 (m, 3H), 1.62 (d, $J_{\text{HH}} = 6.3$ Hz, 3H), 1.37 (s, 9H, 1.13 (t, $J_{\text{HH}} = 7.2$ Hz, 3H); ^1H NMR (DMSO-*d*₆, 500 MHz, 60 °C) δ 10.22 (br s, 2H), 7.66-7.65 (m, 2H), 7.42-7.83 (m, 3H), 4.48 (m, 1H), 4.05 (q, $J_{\text{HH}} = 7.0$ Hz, 2H), 3.78-3.68 (m, 3H), 3.54-3.35 (m, 3H), 1.67 (d, $J_{\text{HH}} = 7.0$ Hz, 3H), 1.36 (s, 9H), 1.13 (t, $J_{\text{HH}} = 7.0$ Hz, 3H); ^{13}C NMR (DMSO-*d*₆, 125.7 MHz, 60 °C) δ 170.20, 152.70, 136.54, 128.68, 128.58, 127.90, 78.95, 60.92, 56.61, 56.00, 47.86, 46.69, 44.70, 27.82, 19.76, 13.50.

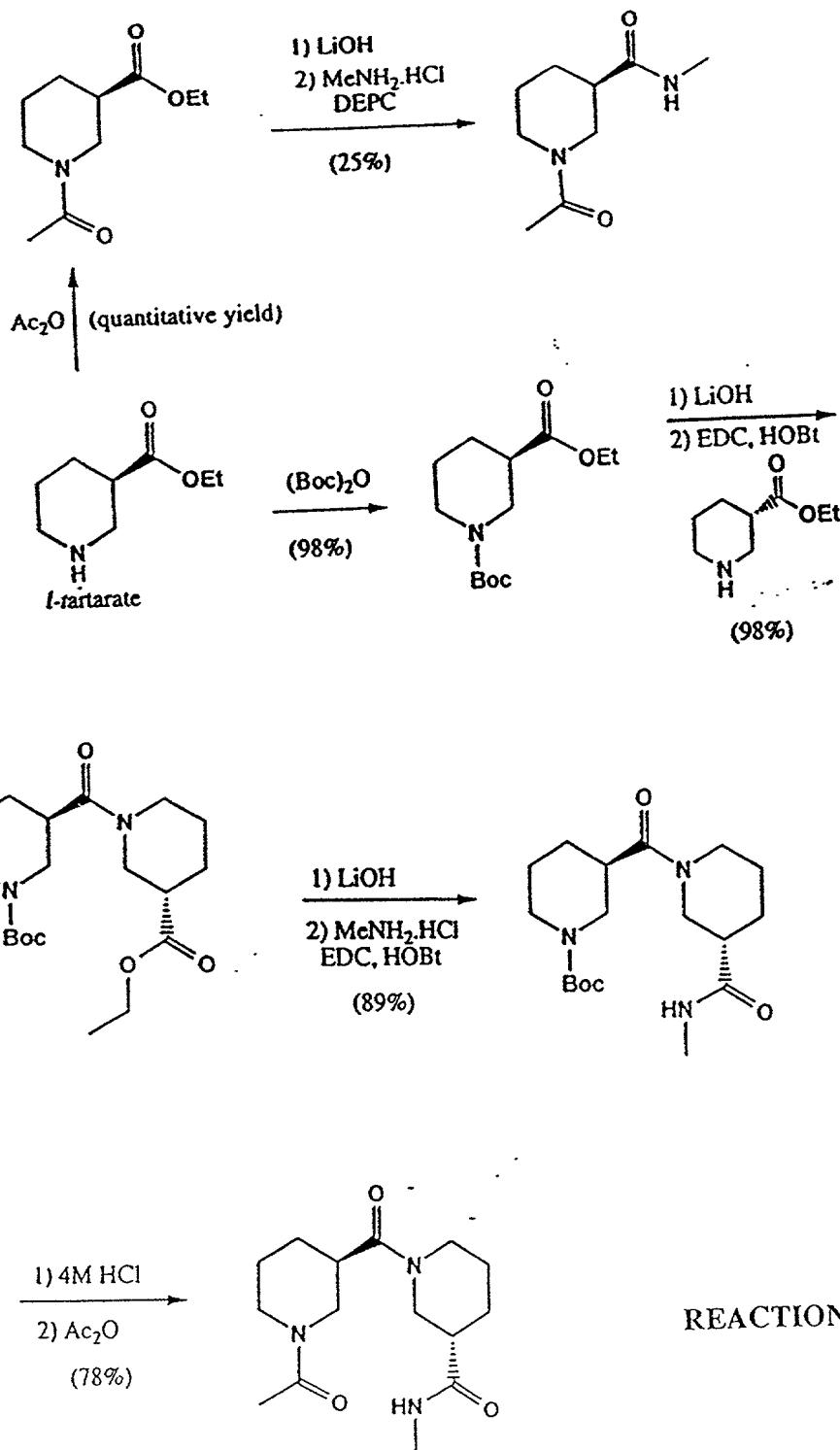
Compound **53a**. A sample of compound **52a** was mixed with excess of saturated Na₂CO₃ solution, extracted into ethyl acetate, dried over MgSO₄ and concentrated *in vacua*. ^1H NMR (CDCl₃, 300 MHz) δ 7.34-7.16 (m, 5H), 4.22-4.07 (m, 2H), 3.80 (q, $J_{\text{HH}} = 6.0$ Hz, 1H), 3.71-3.53 (m, 1H), 3.53-3.22 (m, 3H), 2.94-2.78 (m, 2H), 1.39 (d, rotamer, 9H), 1.32 (d, $J_{\text{HH}} = 6.3$ Hz, 3H), 1.29-1.18 (m, 3H); ^1H NMR (DMSO-*d*₆, 500 MHz, 60 °C) δ 7.35-7.25 (m, 3H), 7.22-7.18 (m, 2H), 4.12-4.05 (m, 2H), 3.78 (q, $J_{\text{HH}} = 7.0$ Hz, 1H), 3.54 (m, 1H), 3.36 (m, 1H), 3.24 (m, 2H), 3.00-2.90 (m, 2H), 1.36 (s, 9H), 1.24 (d, $J_{\text{HH}} = 6.5$ Hz, 3H), 1.54 (t, $J_{\text{HH}} = 7.0$ Hz, 3H); ^{13}C NMR (DMSO-*d*₆, 125.7 MHz, 24 °C) δ 172.57, 172.43, 153.25, 153.14, 145.90, 128.11, 126.60, 126.51, 78.31, 60.28, 58.84, 58.02, 55.61, 51.39, 51.17, 48.53, 47.79, 46.70, 39.33, 24.56, 13.86; ^{13}C NMR (DMSO-*d*₆, 125.7 MHz, 60 °C) δ 172.09, 153.02, 145.72, 127.79, 126.27, 126.21, 78.06, 59.94, 58.43, 55.50, 51.19, 48.28, 46.52, 27.83, 24.12, 13.57; MSMALDI z/e; 363.3 (M±H)

Compound **54a**. Compound **52a** (1.39 g, 3.49 mmol) was dissolved in THF/MeOH/H₂O (6/3/1, v/v/v, 40 mL), and the solution was cooled to 0 °C. LiOH•H₂O (732 mg, 17.4 mmol) was added. The mixture was stirred

at 0 °C for 3 h. Aqueous HCl (1 N, 18 mL) was added at 0 °C. The solvent was then removed on a vacuum rotary evaporator to give a white solid (R_f = 0.32, 1:9 MeOH / CH₂Cl₂). The white solid was dissolved in 150 mL of 95 % ethanol in a hydrogenation flask. Pd-C (10%, 1.1 g) was added. The resulting mixture was shaken under H₂ (45 psi) for 24 h. After the reaction was complete (disappearance of starting material, as monitored by TLC), the mixture was filtered through celite, and the filtrate was concentrated to obtain a white solid. This solid was dissolved in acetone/H₂O (2/1, v/v, 150 mL), cooled to 0 °C, and Fmoc-Osu (1.53 g, 4.54 mmol) and NaHCO₃ (2.93 g, 34.9 mmol) were added. The reaction mixture was stirred at 0 °C for 1 h, and then allowed to stir at room temperature overnight. Water (50 mL) was added. The acetone was removed under reduced pressure. The aqueous layer was stirred for 1 h with diethyl ether (50 mL), the layers were separated and the aqueous layer was acidified with 1 N aqueous HCl, extracted with ethyl acetate, dried over MgSO₄, and concentrated to give a foamy solid. The crude product was purified by crystallization from n-heptane/ethyl acetate to afford 1.13 g (72 %) of 54a as a white solid: mp 113-115 °C, $[\alpha]^{23}_D$ = -18.3 (c 1.2, MeOH); ¹H NMR (CD₃OD, 300 Mhz) δ 7.77 (d, J_{HH} = 7.2 Hz, 2H), 7.62 (d, J_{HH} = 7.5 Hz, 2H), 7.37 (t, J_{HH} = 7.2 Hz, 2H), 7.28 (t, J_{HH} = 7.2 Hz, 2H), 4.48-4.27 (m, 3H), 4.18 (t, J_{HH} = 7.2 Hz, 1H), 3.72-3.46 (m, 3H), 3.14 (m, 1H), 2.88 (m, 1H), 1.44 (s, 9H); ¹³C NMR(CD₃OD, 75.4 MHz, 24 °C) δ 174.63, 158.13, 156.02, 145.24, 145.16, 142.56, 128.74, 128.11, 126.17, 126.10, 120.90, 81.29, 67.77, 54.73, 54.06, 51.73, 51.20, 28.70; ¹³C NMR (CD₃OD, 125.7 MHz, 50 °C) δ 158.20, 156.11, 145.28, 145.22, 142.56, 128.71, 128.09, 126.06, 120.87, 81.12, 67.81, 55.10, 51.61, 28.77; MS-MALDI z/e; 475.3 (M +Na), 491.2 (M + K)

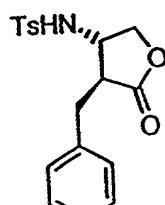
To synthesize the nipecotic reverse turn moiety, Reaction 6 was used.

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To synthesize β -peptides having reverse turn moiety which is a prolyl-glycolic acid residue, the following protocols are preferred:

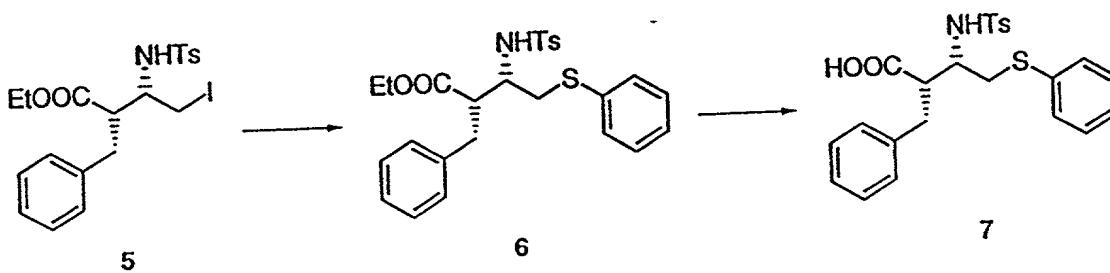
(2S,3R)-3-Amino-2-methylpentanoic acid was prepared according to the procedures given by Jefford and McNulty (1994), *J. Helv. Chim. Acta* 77:2142. However, unlike the description in this paper, the synthesized (2S,3S)-2-methyl-3-(tosylamino)butano-4-lactone contained up to 8% (2R,3S)-2-methyl-3-(tosylamino)butano-4-lactone as a byproduct, which could be removed by recrystallization from toluene. (2S,3S)-3-Amino-2-benzyl-4-phenylthiobutanoic acid was prepared in a synthetic sequence derived from the one by Jefford and McNulty. This synthesis is described below. Homo- α -amino acids were prepared according to the procedures by Podlech and Seebach (1995), *Liebigs Ann.* 1217. Depsi- β -peptides were synthesized by conventional dicyclohexylcarbodiimide / N-hydroxysuccinimide (DCC/HOSu) or 1-ethyl-3-(3'-dimethylaminopropyl)carbodiimide hydrochloride / N,N-dimethyl-4-aminopyridine (EDCI/DMAP) solution-phase coupling procedures (see, for example, Bodanszky, M.; Bodanszky, A. *The Practice of Peptide Synthesis*; Springer Verlag: New York, 1984). Illustrative procedures are given below.



4

(2S,3S)-2-Benzyl-3-(tosylamino)butano-4-lactone (4). A solution of lithium diisopropylamine (LDA) in THF was generated by adding 1.5 M

methyllithium in diethyl ether (30 mL, 45.0 mmol) to a solution of diisopropylamine (6.4 mL, 45.7 mmol) in 100 mL THF at 0°C under nitrogen and stirring for 10 min. The solution was then cooled to -78°C, and a solution of (3S)-3-(tosylamino)butano-4-lactone (5.36 g, 21.1 mmol) in 30 mL THF was added dropwise. The resulting yellow solution was stirred for 1 hour at -78°C, and then benzyl bromide (10 mL, 84.1 mmol) was added rapidly. Stirring at -78°C was continued for 2 hours, and the reaction was quenched with 20 mL sat. aq. NH₄Cl solution and allowed to warm to room temperature. The mixture was acidified with 1 M HCl and extracted three times with methylene chloride. The combined organic extracts were dried over Na₂SO₄ and evaporated to give an orange semisolid that was purified by chromatography (silica gel, hexane/ethyl acetate 3:2) to yield 2.22 g (8.70 mmol, 41%) recovered starting material and 3.37 g (9.76 mmol; 46%) of 4. No diastereomeric addition product could be detected. For further purification 4 can be recrystallized from toluene to give colorless needles. mp. 108.5-109°C, ¹H-NMR (300 MHz, CDCl₃) δ 7.58 (d, J = 8.5 Hz, 2 H), 7.31 (d, J = 8.2 Hz, 2 H), 7.20 (m, 3 H), 6.92 (dd, J = 7.7, 1.7 Hz, 2H), 4.97 (d, J = 5.5 Hz, 1 H), 4.27 (dd, J = 7.2, 9.8 Hz, 1 H), 3.98 (dd, J = 7.2, 9.8 Hz, 1 H), 3.65 (m, 1 H), 3.00 (m, 1 H), 2.77 (m, 2 H), 2.46 (s, 3 H), ¹³C-NMR (75.5 MHz, CDCl₃) δ 144.27 (C), 138.00 (C), 135.83 (C), 129.89 (CH), 128.97 (CH), 128.88 (CH), 127.10 (CH) 71.25 (CH₂) 53.21 (CH), 46.54 (CH), 33.54 (CH₂) 21.50 (CH₃), EI MS m/e 345.1027 calc. for C₁₈H₁₉NO₄S 345.1035.



(2S,3S)-2-Benzyl-4-phenylthio-3-(tosylamino)butanoic acid (7).

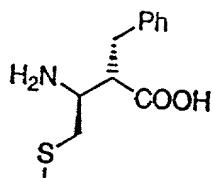
(2S,3S)-2-Benzyl-3-(tosylamino)butano-4-lactone (**4**) (0.91 g, 2.64 mmol) was dissolved in 10 mL methylene chloride. At 0°C trimethylsilyliodide (1 mL, 7.03 mmol) and anhydrous ethanol (0.72 mL, 12.2 mmol) were added under nitrogen. The solution was stirred 30 min. at 0°C, allowed to warm to room temperature and stirred for 1 day. Then the addition of trimethylsilyliodide and ethanol was repeated and stirring at room temperature was continued for 12 hours. The reaction was quenched by the addition of 3 mL ethanol and stirring for 30 min. To the solution 20 mL of water were added, the layers were separated, and the aqueous layer was extracted five times with methylene chloride. The combined organic extracts were washed with 5 % aq. Na₂S₂O₃ solution, dried over Na₂SO₄ and concentrated in vacuo to give 1.78 g of crude **5** as an orange solid, which was used in the next step without further purification.

At 0°C, thiophenol (0.73 ml, 7.11 mmol) was added to a suspension of NaH (289.7 mg, 7.24 mmol) in 6 mL DMF under nitrogen, warmed to room temperature and stirred for 15 min. A solution of crude **5** (1.78 g) in 10 mL DMF was added to the thiophenolate solution at 0°C. After warming to room temperature the solution was stirred for 1 hour. The reaction was quenched with 50 ml water and extracted three times with methylene chloride. The combined organic extracts were washed with brine, dried over Na₂SO₄ and concentrated in vacuo to give 2.43 g of **6** as a colorless oil, which was used in the next step without further purification.

To a solution of **6** (2.43 g) in 18 mL methanol a 1.5 M aq. NaOH solution was added and the mixture heated to 60°C for 2 hours. After evaporation of methanol in vacuo, 20 mL water was added and the mixture extracted two times with diethyl ether. The aqueous layer was acidified with conc. HCl and extracted four times with diethyl ether. The organic extracts were dried over Na₂SO₄ and evaporated to yield 1.04 g (2.28 mmol,

86%) of 7. $^1\text{H-NMR}$ (300 MHz, CDCl_3) δ 7.45 (d, $J = 8.3$ Hz, 2 H), 7.24-7.17 (m, 6 H), 7.09-7.00 (m, 6 H), 5.54 (d, $J = 8.3$ Hz, NH), 3.46 (m, 1 H), 3.28 (m, 1 H), 3.00 (m, 3 H), 2.67 (dd, $J = 7.1, 14.0$ Hz, 1H), 2.34 (s, 3H).

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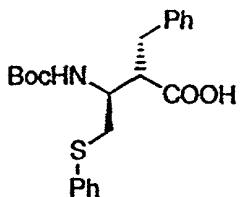
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(2S,3S)-3-Amino-2-Benzyl-4-phenylthiobutanoic acid (8). Compound 7 and phenol (0.77g) were dissolved in 50 mL 48% HBr and heated to reflux for 1.5 hours under nitrogen. After cooling to room temperature 150 mL water was added and the solution extracted two times with diethyl ether. The yellow aqueous layer was evaporated to give 0.58 g of (2S,3S)-3-amino-2-benzyl-4-phenylthiobutanoic acid hydrobromide as an orange solid. $^1\text{H-NMR}$ (300 MHz, CDCl_3) δ 7.69 (b, 3 NH), 7.43 (m, 2 H), 7.34-7.01 (m 8 H), 3.60 (m, 1H), 3.35 (m, 3 H), 3.08 (dd, $J = 8.2, 14.2$ Hz, 1 H), 2.87 (dd, $J = 7.5, 14.2$ Hz, 1 H).

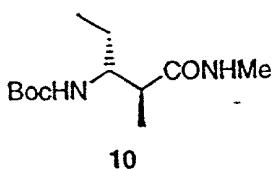
The hydrobromide was dissolved in 140 mL anhydrous ethanol, and 28 mL methyloxirane was added. The solution was heated to reflux for 1 hour under nitrogen. The solvent was evaporated to yield 0.45 g (1.45 mmol, 65 %) of 8.

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(2S,3S)-3-(t-Butoxycarbonylamino)-2-benzyl-4-phenylthiobutanoic acid. To a solution of **8** (0.18 g, 0.597 mmol) in 1 mL water and 2 mL dioxane was added K₂CO₃ (167.9 mg, 1.21 mmol). After cooling to 0°C, di-t-butyl-dicarbonate (153.2 mg, 0.681 mmol) was added, the solution warmed to room temperature and stirred for 1 day. The solution was concentrated in vacuo, and the residue dissolved in 20 mL water. The solution was acidified to pH 2-3 (congo red) with 1 M HCl and extracted five times with ethyl acetate. The combined organic extracts were dried over MgSO₄ and evaporated to give an orange oil that was purified by chromatography (silica gel, hexane/ethyl acetate 1:2) to yield 63.4 mg (0.159 mmol, 27%) of **9**. ¹H-NMR (300 MHz, CDCl₃) δ 7.37-7.13 (m, 10 H), 5.47 (d, J = 8.5 Hz, NH), 3.88 (m, 1 H), 3.20 (m, 1 H), 3.00 (m, 1 H), 2.84 (m, 3 H), 1.39 (s, 9 H), ¹³C-NMR (75.5 MHz, CDCl₃) δ 174.82 (C), 156.49 (C), 140.14 (C), 136.80 (C), 130.44 (C), 130.02 (C), 129.81 (C), 129.36 (C), 127.33 (C), 127.27 (C), 79.68 (C), 52.46 (CH), 52.33 (CH), 37.37 (CH₂), 35.25 (CH₂), 28.55 (3 CH₃).



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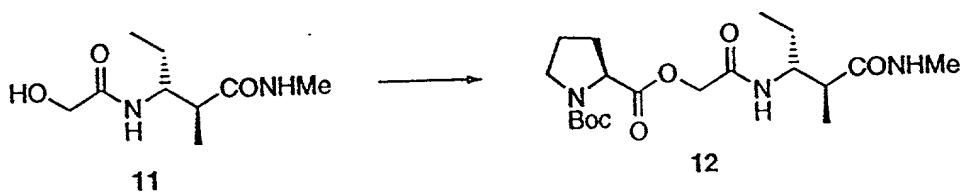
Methyl-(2S,3R)-3-(t-butoxycarbonylamino)-2-methylpentanoic amide (**10**). (2S,3R)-3-(t-Butoxycarbonylamino)-2-methylpentanoic acid

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(149.1 mg, 0.645 mmol) was dissolved in 1 mL DMF. At 0°C methylamine hydrochloride (88.6 mg, 1.31 mmol) and DMAP (195.7 mg, 1.60 mmol) were added, followed by EDCI (1-ethyl-3-(3'-dimethylaminopropyl)carbodiimide hydrochloride) (376.9 mg, 1.97 mmol). After stirring at room temperature for 2 days, the solvent was removed in a stream of nitrogen and the residue dried in vacuo. The residue was titurated with 1 mL 1 M HCl and 4 mL water, and the white precipitate was collected by suction filtration to yield 121.0 mg (0.495 mmol, 66%) of the amide **10** mp. 206-207°C, ¹H-NMR (300 MHz, CDCl₃) δ 5.92 (b, NH), 4.72 (b, NH), 3.58 (m, 1 H), 2.77 (d, J = 4.8 Hz, 3 H), 2.45 (m, 1 H), 1.45 (m, 1 H), 1.41 (s, 9 H), 1.40 (m, 1 H), 1.13 (d, J = 7.2 Hz, 3 H), 0.90 (t, J = 7.4 Hz, 3 H), ¹³C-NMR (75.5 MHz, CDCl₃) δ 174.83 (C), 156.15 (C), 79.35 (C), 54.62 (CH), 45.02 (CH), 28.35 (3 CH₃), 26.24 (CH₃), 25.18 (CH₂), 13.71 (CH₃), 10.85 (CH₃), EI MS m/e 244.1789 calc. for C₁₂H₂₄N₂O₃ 244.1787.



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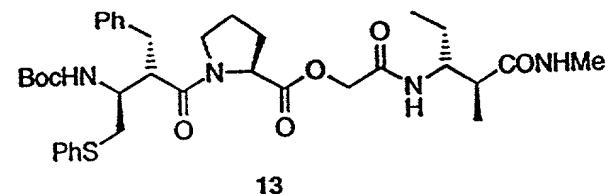
Compound 12. Compound **10** (121.0 mg, 0.495 mmol) was dissolved in 2 mL of 4 M HCl/dioxane, and the resulting solution was stirred 1 hour at room temperature. HCl/dioxane was then removed in a stream of nitrogen and the deprotected amide dried in vacuo. The activated glycolic ester was prepared by adding EDCI (188.7 mg, 0.635 mmol) to a solution of glycolic acid (45.5 mg, 0.598 mmol) and HOSu (N-

hydroxysuccinimide) (72.7 mg, 0.632 mmol) in 1 mL DMF and stirring of the solution at room temperature for 2 hours. The deprotected amide and triethylamine (85 μ l, 0.610 mmol) were dissolved in 1 mL DMF and transferred into the activated ester solution. After stirring the resulting solution for 2 days at room temperature, the solvent was removed in a stream of nitrogen and the residue dried in vacuo. The residue was separated by chromatography (silica gel, CHCl₃/MeOH 4:1) to yield impure 11 (192.7 mg), which was used in the next step without further purification.

Compound 11 (192.7 mg) and BOC-L-proline (213.3 mg, 0.991 mmol) were dissolved in 3 mL DMF. DMAP (15.6 mg, 0.128 mmol) was added, followed by DCC (dicyclohexylcarbodiimide) (248.3 mg, 1.20 mmol), and the resulting solution was stirred overnight at room temperature. The white precipitate was filtered off by suction filtration, and the filtrate was concentrated in vacuo. The residue was separated by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 145.7 mg (0.365 mmol, 74 % based on 10) of 12. ¹H-NMR (300 MHz, CDCl₃) δ 7.02 (d, J = 8.6 Hz, NH major rotamer 89 %), 6.91 (d, J = 9.0 Hz, NH minor rotamer 11 %), 6.10 (m, NH), 4.78 (AB, A part, J = 15.3 Hz, 1 H), 4.49 (AB, B part, J = 15.3 Hz, 1 H) 4.26 (m, 1 H), 3.90 (m, 1 H), 3.44 (m, 2 H), 2.74 (d, J = 4.6 Hz, 3 H), 2.45 (quint., J = 7.0 Hz, 1 H), 2.22 (m, 1 H), 1.98 (m, 2 H), 1.88 (m, 1 H), 1.56 (m, 1 H), 1.43 (s, 9 H), 1.43 (m, 1 H), 1.08 (d, J = 7.0 Hz, 3 H), 0.86 (t, J = 7.4 Hz), ¹³C-NMR (75.5 MHz, CDCl₃) δ 174.80 (C), 172.24 (C), 167.47 (C), 154.78 (C), 80.33 (C), 62.79 (CH₂), 58.77 (CH), 53.74 (CH), 46.75 (CH₂), 45.58 (CH), 29.91 (CH₂), 28.26 (3 CH₃), 26.05 (CH₃), 24.97 (CH₂), 24.49 (CH₂), 14.43 (CH₃), 10.62 (CH₃).

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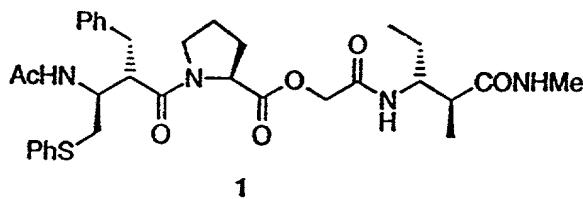
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Compound 13. Compound **12** (12.3 mg, 30.8 μmol) was dissolved

in 1 mmol 4 M HCl/dioxane and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and (2S,3S)-2-benzyl-3-(t-butoxycarbonylamino)-4-phenylthiobutanoic acid (**9**) (14.3 mg, 35.6 μmol) were dissolved in 0.5 mL methylene chloride. DMAP (5.0 mg, 40.9 μmol) was added, followed by EDCI (13.7 mg, 71.5 μmol). After stirring at room temperature for 2 days, the solvent was removed in a stream of nitrogen and the residue dried in vacuo. The residue was titurated with 1 mL water, which was acidified to pH 2. The resulting solid was collected and purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 14.1 mg (20.6 μmol , 67%) of **13**. ¹H-NMR (300 MHz, CDCl₃) δ 7.41 (d, J = 10.1 Hz, NH), 7.38-7.13 (m, 10 H + NH), 5.06 (AB, A part, J = 15.3 Hz, 1 H), 5.03 (d, J = 10.5 Hz, NH), 4.45 (m, 1 H), 4.32 (AB, B part, J = 15.5 Hz, 1 H), 4.26 (m, 1 H), 4.02 (t, J = 7.6 Hz, 1 H), 3.31 (m, 1 H), 3.08 (m, 3 H), 2.97 (m, 1 H), 2.83 (m, 1 H), 2.78 (d, J = 4.6 Hz, 3 H), 2.53 (m, 1 H), 2.39 (dq, J = 10.1 Hz, 6.9 Hz, 1 H), 1.98 (m, 1 H), 1.73 (m, 2H), 1.50 (m, 1 H), 1.44 (m, 1 H), 1.41 (s, 9 H), 1.30 (m, 1 H), 1.07 (d, J = 6.9 Hz, 3 H), 0.98 (t, J = 7.4 Hz, 3 H), ¹³C-NMR (75.5

MHz, CDCl₃) δ 175.44 (C), 171.63 (C), 167.03 (C), 155.54 (C), 138.29 (C), 135.46 (C), 129.43 (CH), 129.06 (CH), 128.68 (CH), 128.30 (CH), 126.60 (CH), 126.47 (CH), 80.24 (C), 62.69 (CH₂), 59.27 (CH), 52.71 (CH), 52.46 (CH), 49.39 (CH), 46.75 (CH₂), 46.66 (CH), 38.16 (CH₂), 36.32 (CH₂), 28.58 (CH₂), 28.11 (3 CH₃), 26.26 (CH₂), 25.85 (CH₃), 25.05 (CH₂), 16.22 (CH₃), 10.47 (CH₃).
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Compound 1. Compound 13 (14.1 mg, 20.6 μmol) was dissolved in 1 mL 4 M HCl/dioxane and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and triethylamine (5.8 μL, 41.6 μmol) were dissolved in 0.41 mL methylene chloride, and acetic anhydride (2.4 μL, 25.4 μmol) was added. After stirring the solution at room temperature overnight the solvent was removed in a stream of nitrogen and the residue dried in vacuo. The residue was purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 9.2 mg (14.7 μmol, 71%) of 1. mp. 196.5-197°C, ¹H-NMR (300 MHz, CDCl₃) δ 7.40 (d, J = 9.0 Hz, NH), 7.39-7.11 (m, 10 H + NH), 5.99 (d, J = 10.1 Hz, NH), 5.03 (AB, A part, J = 15.3 Hz, 1 H), 4.78 (tt, J = 10.3 Hz, 3.6 Hz,

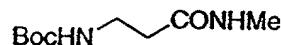
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1 H), 4.34 (AB, B part, $J = 15.3$ Hz, 1 H), 4.25 (dq, $J = 10.0$ Hz, 1 H), 4.02 (t, $J = 7.4$ Hz, 1 H), 3.36 (m, 1 H), 3.20-3.00 (m, 3 H), 2.85-2.75 (m, 2 H), 2.79 (d, $J = 4.6$ Hz, 3 H), 2.60 (m, 1 H), 2.42 (dq, $J = 10.1$ Hz, 6.9 Hz, 1 H), 2.00 (m, 1 H), 1.86 (s, 3 H), 1.85-1.62 (m, 3 H), 1.52 (m, 1 H), 1.31 (m, 1 H), 1.07 (d, $J = 6.8$ Hz, 3 H), 0.97 (t, $J = 7.4$ Hz, 3 H), ^{13}C -NMR (75.5 MHz, CDCl_3) δ 175.46 (C), 171.59 (C), 170.17 (C), 167.08 (C), 138.14 (C), 136.87 (C), 135.36 (C), 129.49 (CH), 129.15 (CH), 128.60 (CH), 128.34 (CH), 126.88 (CH), 126.64 (CH), 62.69 (CH₂), 59.30 (CH), 52.80 (CH), 51.08 (CH), 48.69 (CH), 46.83 (CH₂), 46.28 (CH), 37.37 (CH₂), 36.30 (CH₂), 34.45 (CH₂), 28.59 (CH₂), 26.03 (CH₃), 25.07 (CH₂), 23.00 (CH₃), 16.09 (CH₃), 10.46 (CH₃), IR (1 mM in CH_2Cl_2) 3423, 3367, 1753, 1669, 1626 cm^{-1} , EI MS m/e 624.2989 calc. for $\text{C}_{33}\text{H}_{44}\text{N}_4\text{O}_6\text{S}$ 624.2981.



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Methyl-3-(t-butoxycarbonylamino)propionic amide (14). BOC- β -alanine (0.50 g, 2.64 mmol) was dissolved in 4 mL DMF. Methylamine hydrochloride (198 mg, 2.93 mmol) and DMAP (427.2 mg, 3.50 mmol) were added, followed by EDCI (1.06 g, 5.53 mmol). After stirring at room temperature for 2 days the solvent was removed in a stream of nitrogen and the residue dried in vacuo. It was dissolved in 5 mL 1 M HCl, and the solution was extracted five times with ethyl acetate. The combined organic

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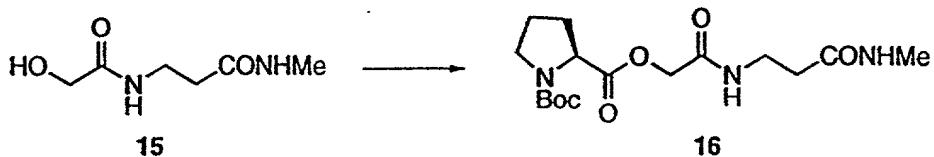
extracts were dried over MgSO_4 and concentrated to yield 0.43 g (2.13 mmol, 81 %) of BOC- β -alanine methylamide (**14**) as a white solid. mp. 117–118 °C, $^1\text{H-NMR}$ (300 MHz, CDCl_3) δ 5.78 (b, NH), 5.15 (b, NH), 3.38 (q, J = 6.1 Hz, 2 H), 2.78 (d, J = 4.8 Hz, 3 H), 2.36 (t, J = 6.1 Hz, 2 H), 1.40 (s, 9 H) $^{13}\text{C-NMR}$ (75.5 MHz, CDCl_3) δ 171.74 (C), 79.15 (C), 36.41 (CH_2), 36.03 (CH_2), 28.17 (3 CH_3), 26.04 (CH_3).

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Compound 16. Compound **14** (0.33 g, 1.63 mmol) was dissolved in 5 mL of 4 M HCl/dioxane, and the solution was stirred at 12 °C for 1 hour. The HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. An activated ester solution was prepared by adding DCC (509.9 mg, 2.47 mmol) to a solution of glycolic acid (145.7 mg, 1.92 mmol) and HOSu (326.4 mg, 2.84 mmol) in 10 mL methylene chloride. A white precipitate formed after a few minutes. The suspension was stirred at 12 °C for 6 hours. The deprotected amide and triethylamine (0.27 mL, 1.94 mmol) were dissolved in 10 mL methylene chloride and transferred into the activated ester solution. After stirring the resulting solution overnight at room temperature, the white precipitate was filtered off by suction filtration and the filtrate concentrated to give a white solid, which was purified by chromatography (silica gel, $\text{CHCl}_3/\text{MeOH}$ 19:1) to yield 0.30 g of impure **15**, which was used in the next step without further purification.

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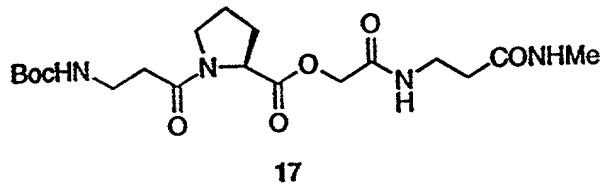
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Compound **15** (0.30 g) and BOC-L-proline (371.5 mg, 1.73 mmol) were dissolved in 50 mL methylene chloride. At 0°C DMAP (25.6 mg, 0.210 mmol) was added, followed by DCC (402.9 mg, 1.95 mmol). After stirring 1 hour at 0°C the suspension was allowed to warm to room temperature and stirred overnight. The white precipitate was filtered off by suction filtration and the filtrate concentrated. The residue was subjected to chromatography (silica gel, CHCl₃/MEOH 19:1) to yield 0.23 g (0.644 mmol, 40% based on **14**) of **15** as a colorless glass. ¹H-NMR (300 MHz, CDCl₃) δ 7.55 (b, NH major rotamer 84%), 7.05 (b, NH minor rotamer 16%), 6.25 (b, NH major rotamer 83%), 6.04 (b, NH, minor rotamer 17%), 4.59 (s, 2 H), 4.25 (m, 1 H), 3.59 (m, 1 H), 3.42 (m, 3 H), 2.73 (d, J = 4.8 Hz, 3 H), 2.41 (t, J = 6.5 Hz, 2 H), 2.22 (m, 1 H), 1.96 (m, 2 H), 1.88 (m, 1 H), 1.42 (s, 9 H).



Compound 17. Compound **16** (0.23 g, 0.644 mmol) was dissolved in 2 mL 4 M HCl/dioxane, and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and BOC-β-alanine (133.3 mg, 0.705 mmol) were dissolved in 5 mL methylene chloride. DMAP (96.9 mg, 0.793 mmol) was added, followed by EDCI (258.7 mg, 1.349 mmol). After stirring at room temperature for 2 days the solvent was removed in a stream of nitrogen. The residue was dissolved in 0.1 M HCl and the solution was extracted four times with methylene chloride. The combined organic extracts were dried over MgSO₄ and concentrated to give

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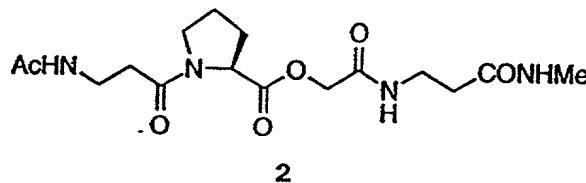
a white solid that was purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 0.18 g (0.420 mmol, 66%) of 17 as a white solid. ¹H-NMR (300 MHz, CDCl₃) δ 7.54 (b, NH), 6.30 (b, NH), 5.58 (b, NH), 4.66 (AB, A part, J = 15.4 Hz, 1 H), 4.47 (AB, B part, J = 15.5 Hz, 1 H), 4.35 (m, 1 H), 3.51 (m, 4 H), 3.35 (m, 2 H), 2.72 (d, J = 4.8 Hz, 3 H), 2.51 (m, 2 H), 2.41 (m, 2 H), 2.20 (m, 1 H), 2.10 (m, 1 H), 1.98 (m, 2 H), 1.37 (s, 9 H).

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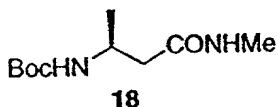


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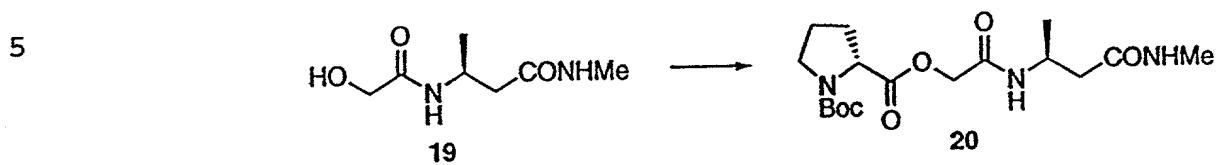
Compound 2. Compound 17 (0.18 g, 0.420 mmol) was dissolved in 2 mL 4 M HCl/dioxane and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and triethylamine (0.12 mL, 0.861 mmol) were dissolved in 5 mL methylene chloride. At 0°C acetic anhydride (50 μL, 0.530 mmol) was added and the solution was stirred 1 hour at 0°C and then allowed to warm to room temperature with stirring overnight. The solvent was removed in a stream of nitrogen and the residue dried in vacuo. The remaining white solid was purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 0.12 g (0.324 mmol, 77%) of 2 as a white solid. mp. 153.5-154°C, ¹H-NMR (300 MHz, CDCl₃) 7.79 (d, J = 4.4 Hz, NH), 7.32 (d, J = 3.9 Hz, NH), 6.08 (b, NH), 4.75 (AB, A part, J 15.4 Hz, 1 H), 4.44 (AB, B part, J = 15.3 Hz, 1 H), 4.32 (m, 1 H), 3.62-3.40 (m, 5 H), 2.74 (d, J = 4.8 Hz, 3 H), 2.59-2.34 (m, 4 H), 2.25-1.91 (m, 3 H), 1.97 (s, 3 H), ¹³C-NMR (75.5 MHz, CDCl₃) δ 171.57 (C), 171.30 (C), 170.63 (C), 167.42 (C), 62.78 (CH₂),

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59.10 (CH), 47.02 (CH₂), 35.83 (CH₂), 35.54 (CH₂), 34.69 (CH₂), 33.75 (CH₂), 29.00 (CH₂), 26.17 (CH₃), 25.05 (CH₂), 22.83 (CH₃), IR (1 mM in CH₂C₁₂) 3452, 3334, 1757, 1669, 1635, 1539 cm⁻¹, EI MS m/e 370.1868 calc. for C₁₆H₂₆N₄O₆ 370.1852.



Methyl-(S)-3-(t-butoxycarbonylamino)butanoic amide (**18**). BOC-homoalanine (Podlech, J.; Seebach, D. (1995) *Liebigs Ann.* 1217) (0.44 g, 2.17 mmol) was dissolved in 5 mL methylene chloride. HOSu (376.4 mg, 3.27 mmol) was added and the solution cooled to 0°C. After addition of DCC (587.8 mg, 2.85 mmol) the solution was stirred 1 hour at 0°C, warmed to room temperature and stirred for an additional 2 hours. A stream of methylamine was bubbled through the suspension for 10 minutes, and stirring was continued overnight. The white precipitate was filtered off by suction filtration and the filtrate concentrated to give a pale yellow solid that was purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 0.41 g (1.90 mmol, 88 %) Of BOC-homoalanine methylamide (**18**) as a white solid. ¹H-NMR (300 MHz, CDCl₃) δ 6.11 (b, NH), 5.23 (b, NH), 3.92 (m, 1 H), 2.75 (d, J = 4.8 Hz, 3 H), 2.35 (m, 2 H), 1.39 (s, 9 H), 1.17 (d, J = 6.6 Hz, 3 H).



Compound 20. Compound **18** (0.41 g, 1.90 mmol) was dissolved in 2 mL of 4 M HCl/dioxane, and the solution was stirred at room temperature for 1 hour. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. An activated ester solution was prepared by adding DCC (0.59 g, 2.86 mmol) to a solution of glycolic acid (175.5 mg, 2.31 mmol) and HOSu (421.9 mg, 3.67 mmol) in 5 mL DMF at 0°C. The suspension was stirred at 0°C for 1 hour and then 2 hours at room temperature. The deprotected amide and triethylamine (0.32 mL, 2.30 mmol) were dissolved in 5 mL DMF and transferred into the activated ester solution. After stirring the resulting solution overnight at room temperature the white precipitate was filtered off by suction filtration and the filtrate concentrated to give a semisolid that was chromatographed (silica gel, CHCl₃/MeOH 9:1) to yield 0.42 g of impure **19**, which was used in the next step without further purification.

Compound 19 (55 mg, 0.317 mmol, impure) and BOC-D-proline (148 mg, 0.688 mmol) were dissolved in 2 mL DMF. DMAP (10.0 mg, 0.082 mmol) was added, followed by DCC (171.4 mg, 0.831 mmol). After stirring the resulting suspension for 1 day at room temperature the white precipitate was filtered off by suction filtration and the filtrate concentrated. The remaining semisolid was purified by chromatography (silica gel,

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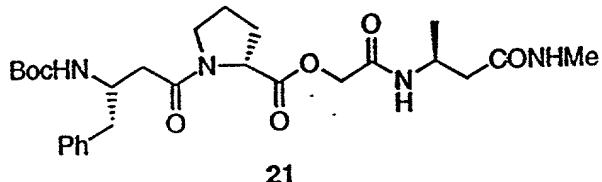
$\text{CHCl}_3/\text{MeOH}$ 19:1) to yield 52.1 mg (0.140 mmol, 44%) of **20**. $^1\text{H-NMR}$ (300 MHz, CDCl_3) δ 7.53 (d, $J = 6.3$ Hz, NH minor rotamer 21%), 7.30 (d, $J = 7.4$ Hz, NH major rotamer 79%), 6.35 (b, NH major rotamer 84%), 6.13 (b, NH minor rotamer 16%), 4.74 (AB, A Part, $J = 15.4$ Hz, 1 H), 4.44 (AB, B part, $J = 15.4$ Hz, 1 H), 4.28 (m, 2 H), 3.45 (m, 2 H), 2.72 (d, $J = 4.8$ Hz, 3 H), 2.41 (dA-B, A part, $J = 7.4$ Hz, 14.3 Hz, 1 H), 2.31 (dAB, B part, $J = 5.3$ Hz, 14.3 Hz, 1 H), 2.23 (m, 1 H), 1.98 (m, 2 H), 1.88 (m, 1 H), 1.43 (s, 9 H), 1.25 (d, $J = 6.8$ Hz, 3 H).

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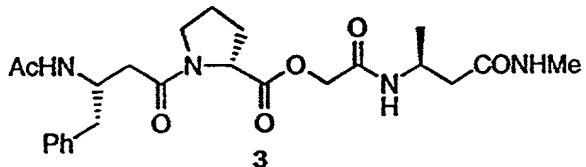
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Compound 21. Compound **20** (52.1 mg, 0.140 mmol) was dissolved in 1 mL 4 M HCl/dioxane and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and BOC-homophenylalanine (42.5 mg, 0.152 mmol) were dissolved in 5 mL methylene chloride. DMAP (32.4 mg, 0.265 mmol) was added, followed by EDCI (59.4 mg, 0.310 mmol). After stirring at room temperature for 2 days the solvent was removed in a stream of nitrogen. The residue was dissolved in 0.1 M HCl, and the solution was extracted three times with methylene chloride. The combined organic extracts were dried over MgSO_4 and concentrated to give a colorless glass that was purified by chromatography (silica gel, $\text{CHCl}_3/\text{MeOH}$ 19:1) to yield 62.8 mg (0.118 mmol, 84%) of **21**. $^1\text{H-NMR}$ (300 MHz, CDCl_3) δ 7.36 (b, NH), 7.31-7.12 (m, 5 H), 6.43 (b, NH), 5.22 (b, NH), 4.82 (AB, A part, $J = 14.9$ Hz, 1 H), 4.49 (m, 2 H), 4.41 (AB, B part, $J = 15.6$ Hz, 1 H), 4.21 (m, 1 H), 3.52 (m, 1 H), 3.32 (m, 1 H), 2.89 (m, 1 H), 2.78 (m, 1 H), 2.71 (d,

J = 4.8 Hz, 3 H), 2.46 (m, 3 H), 2.40 (m, 1 H), 2.24 (m, 1 H), 2.12-1.89
(m, 3 H), 1.38 (s, 9 H), 1.25 (d, J = 6.8 Hz, 3 H).

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Compound 3. Compound **21** (62.8 mg, 0.118 mmol) was dissolved in 1 mL 4 M HCl/dioxane and the solution was stirred for 1 hour at room temperature. HCl/dioxane was removed in a stream of nitrogen and the residue dried in vacuo. The deprotected depsipeptide and triethylamine (90 μ L, 0.646 mmol) were dissolved in 1 mL methylene chloride. At 0°C acetic anhydride (35 μ L, 0.371 mmol) was added and the solution was stirred 1 hour at 0°C and then allowed to warm to room temperature with stirring overnight. The solvent was removed in a stream of nitrogen and the residue dried in vacuo. The residue was purified by chromatography (silica gel, CHCl₃/MeOH 19:1) to yield 52.1 mg (0.110 mmol, 93 %) of **3**. mp. 128-129°C, ¹H-NMR (300 MHz, CDCl₃) δ 7.49 (d, J = 8.5 Hz, NH), 7.31-7.16 (m, 5 H), 6.80 (d, J = 8.5 Hz, NH), 6.35 (m, NH), 4.73 (AB, A part, J = 15.1 Hz, 1 H), 4.49 (m, 1 H), 4.45 (AB, B part, J = 15.4 Hz, 1 H), 4.38 (m, 2 H), 3.55 (m, 1 H), 3.28 (m, 1 H), 2.99 (dAB, A part, J = 6.2 Hz, 13.4 Hz, 1 H), 2.88 (dAB, B part, J = 8.5 Hz, 13.6 Hz, 1 H), 2.72 (d, J = 4.8 Hz, 3 H), 2.55 (dAB, A part, J = 5.2 Hz, 15.6 Hz, 1 H), 2.43 (dAB, B part, J = 5.9 Hz, 15.5 Hz, 1 H), 2.45 (d, J = 6.3 Hz, 2 H), 2.25 (m, 1 H), 2.21 - 1.89 (m, 3 H), 1.93 (s, 3 H), 1.26 (d, J = 6.6 Hz, 3 H), ¹³C-NMR (75.5 MHz CDCl₃) δ 170.90 (C), 170.31 (C), 169.75 (C), 128.93 (CH), 128.32 (CH), 126.40 (CH), 62.60 (CH₂), 58.89 (CH), 47.31 (CH₂), 42.44 (CH, CH₂), 39.57 (CH₂), 36.22 (CH₂), 28.92 (CH₂), 25.96

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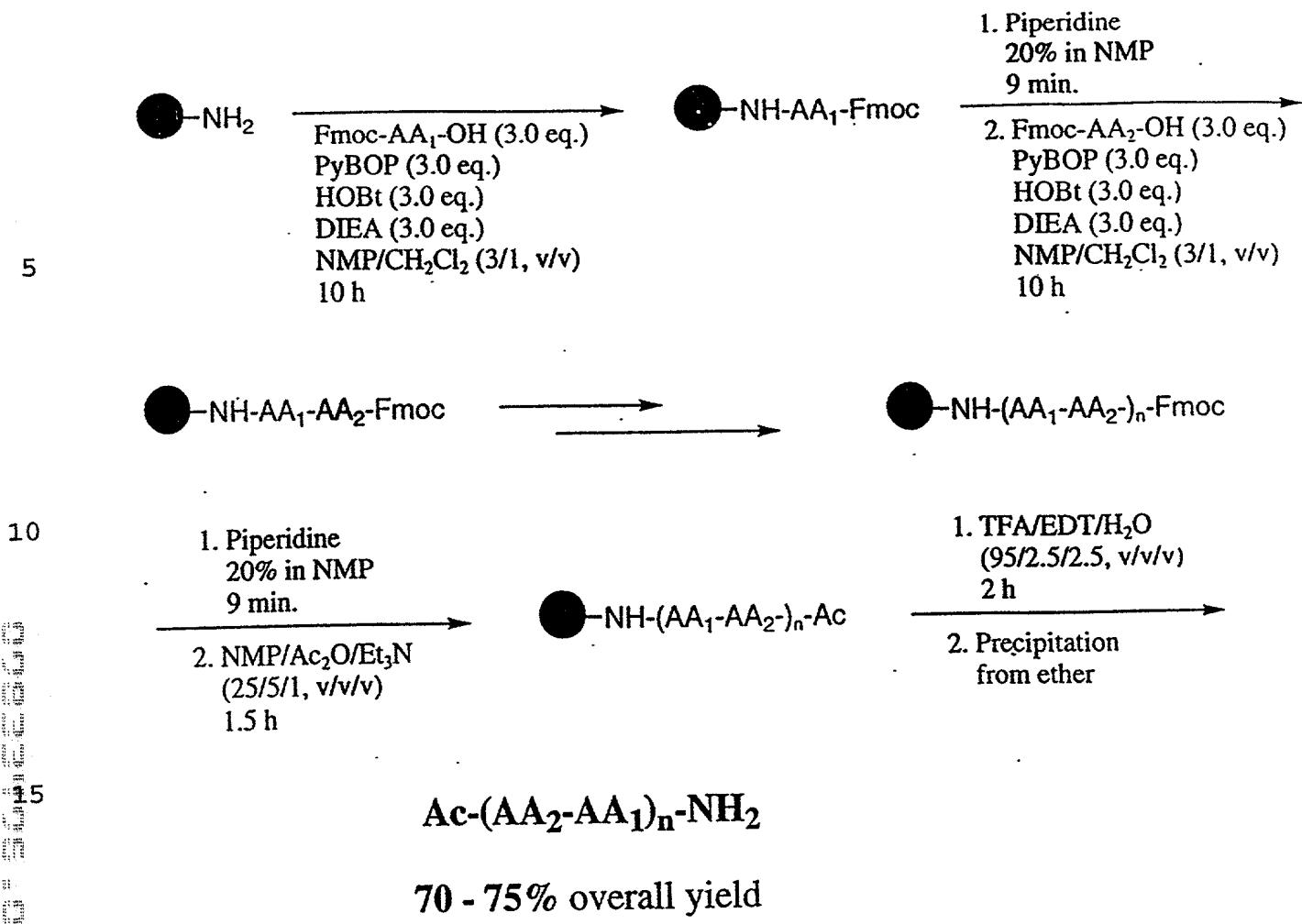
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(CH₃), 24.94 (CH₂), 23.02 (CH₃), 20.21 (CH₃), IR (1 mM in CH₂Cl₂) 3452, 3433, 3346 cm⁻¹, EI MS m/e 474.2474 calc. for C₂₄H₃₄N₄O₆ 474.2478.

Construction of polypeptides using any type of β -amino acid can be accomplished using conventional and widely recognized solid-phase or solution-phase synthesis. Very briefly, in solid-phase synthesis, the desired C-terminal amino acid residue is linked to a polystyrene support as a benzyl ester. The amino group of each subsequent amino acid to be added to the N-terminus of the growing peptide chain is protected with Boc, Fmoc, or another suitable protecting group. Likewise, the carboxylic acid group of each subsequent amino acid to be added to the chain is activated with DCC and reacted so that the N-terminus of the growing chain always bears a removable protecting group. The process is repeated (with much rinsing of the beads between each step) until the desired polypeptide is completed. In the classic route, the N-terminus of the growing chain is protected with a Boc group, which is removed using trifluoracetic acid, leaving behind a protonated amino group. Triethylamine is used to remove the proton from the N-terminus of the chain, leaving a the free amino group, which is then reacted with the activated carboxylic acid group from a new protected amino acid. When the desired chain length is reached, a strong acid, such as hydrogen bromide in trifluoracetic acid, is used to both cleave the C-terminus from the polystyrene support and to remove the N-terminus protecting group.

The preferred solid-phase synthesis used herein is shown in Reaction 7:



REACTION 7

AA_n = incoming amino acid to be added to chain

Fmoc = the protecting group 9-fluorenylmethyloxycarbonyl

NMP = N-methyl pyrrolidone

EDT = Ethanedithiol

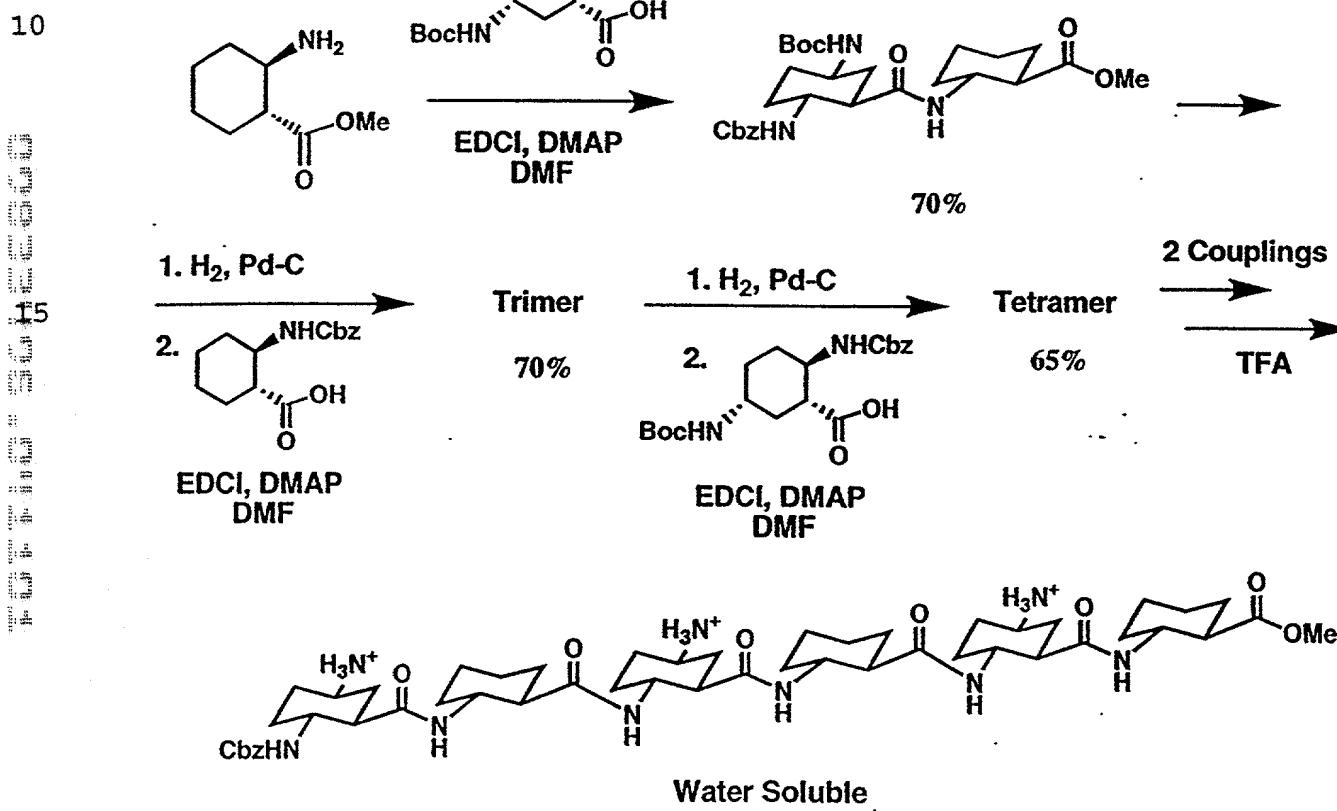
25 PyBOP = benzotriazol-1-yloxytritypyrrolidinophosphonium hexafluorophosphate

HOBT = N-hydroxy-benzotriazole

DIEA = diisopropylethyl amine

Solid-phase peptide synthesis is widely employed and well known. Consequently, it will not be described in any further detail here.

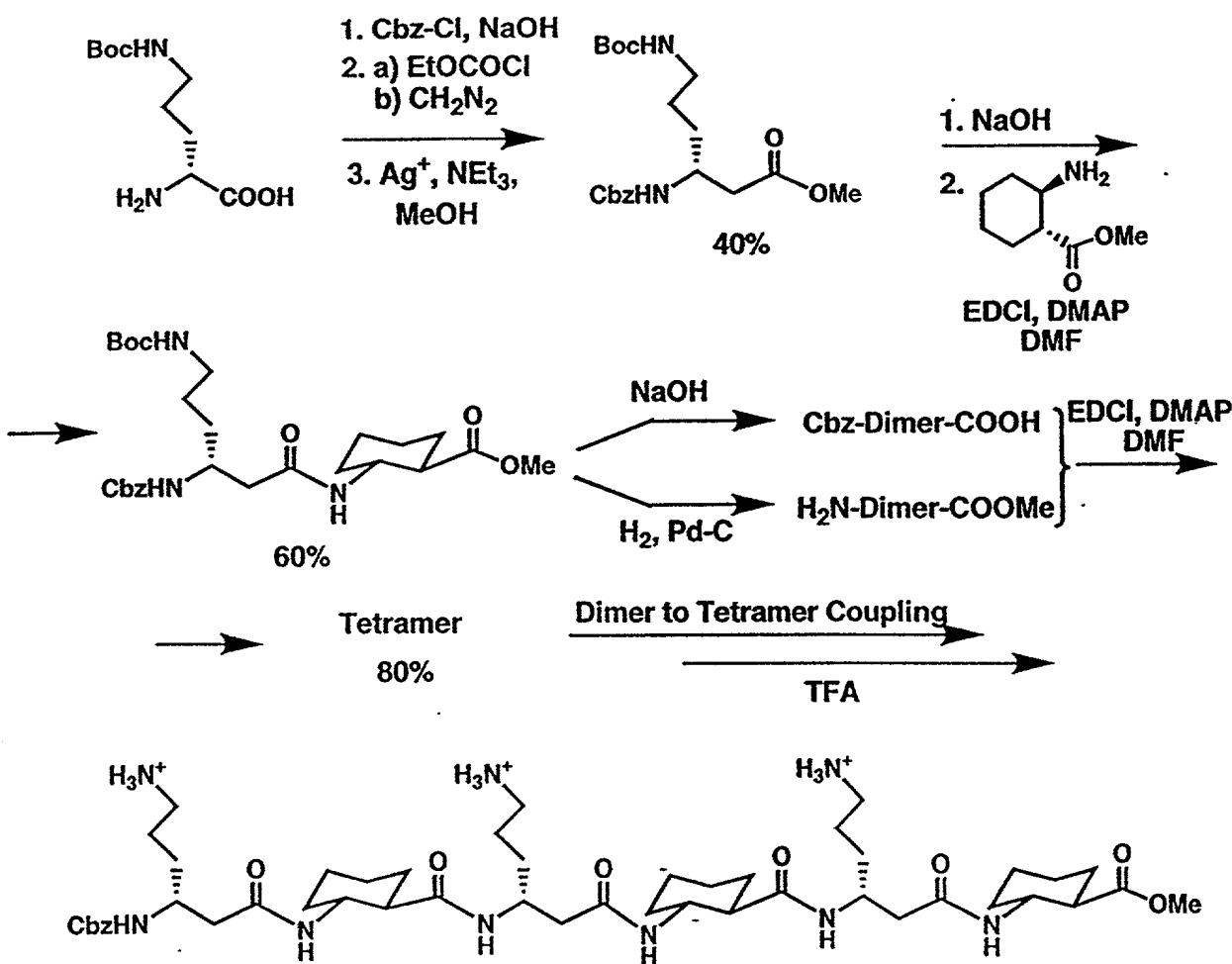
Solution phase synthesis, noted above, can also be used with equal success. For example, solution-phase synthesis of a β -peptide chain containing alternating residues of unsubstituted cyclohexane rings and amino-substituted cyclohexane rings proceeds in conventional fashion as outlined in Reaction 8:



REACTION 8

Reaction 8 works with equal success to build peptides wherein the residues are the same or different.

Reaction 9 is an illustration of a homologation reaction combined with conventional solution-phase peptide synthesis which yields a β -peptide having acyclic-substituted residues alternating with ring-constrained residues:



REACTION 9

As noted above, the β -peptides of the present invention can be substituted with any number of substituents, including hydroxy, linear or branched C₁-C₆-alkyl, alkenyl, alkynyl; hydroxy-C₁-C₆-alkyl, amino-C₁-C₆-alkyl, C₁-C₆-alkyloxy, C₁-C₆-alkyloxy-C₁-C₆-alkyl, amino, mono- or di-C₁-C₆-alkylamino, carboxamido, carboxamido-C₁-C₆-alkyl, sulfonamido, sulfonamido-C₁-C₆-alkyl, urea, cyano, fluoro, thio, C₁-C₆-alkylthio, mono- or bicyclic aryl, mono- or bicyclic heteraryl having up to 5 heteroatoms selected from N, O, and S; mono- or bicyclic aryl-C₁-C₆-alkyl, heteroaryl-C₁-C₆-alkyl, and combinations thereof. Effecting such substitutions is well within the set of skills possessed by a synthetic peptide chemist.

For example, appending a sulfonamido moiety to the cyclic backbone substituent can be accomplished in conventional fashion using Reaction 10.

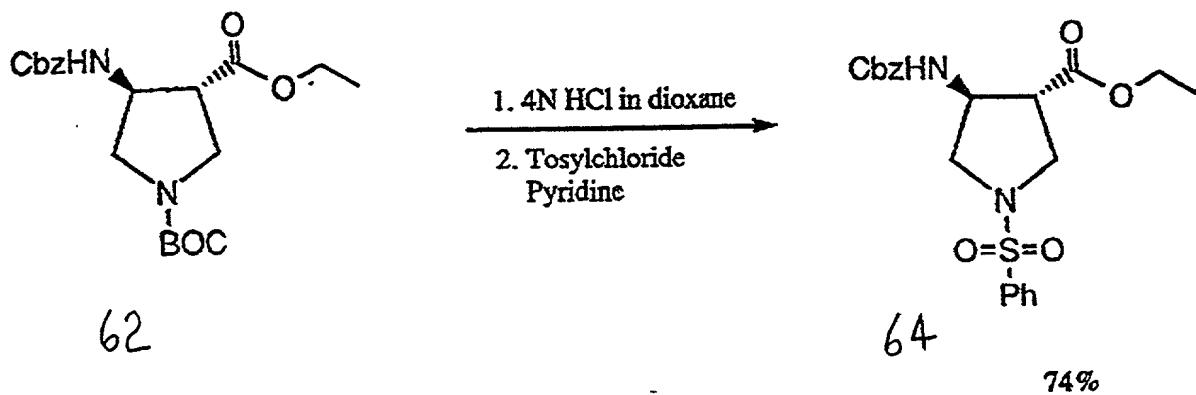
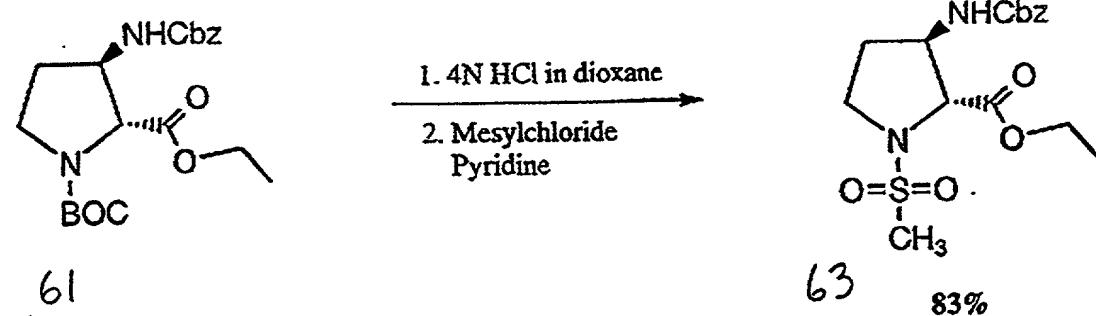
Compound 63: Compound **61** (90 mg) was dissolved in 4 N HCl in dioxane (2.0 ml). The reaction mixture was stirred for 1.5 hours. The dioxane was then removed *in vacuo*. The residue was dissolved in pyridine (2.0 ml), then cooled to 0° C in an ice-bath.

Methanesulfonylchloride (71 μ I) was added dropwise. After the addition, the reaction mixture was stirred at room temperature for 12 hours. The pyridine was then removed *in vacuo*. The residue was taken up in ethyl acetate (50 ml). The mixture was washed with dilute brine (2 x 10 ml), dried over MgSO₄, and concentrated to give the clean product as a colorless oil (70 mg) in 82% yield.

Compound 64: Compound **62** (30 mg) was dissolved in 4 N HCl in dioxane (2.0 ml). The reaction mixture was stirred for 1.5 hours. The dioxane was then removed *in vacuo*. The residue was dissolved in pyridine (1.0 ml), then cooled to 0° C in an ice-bath. Toluenesulfonylchloride (63 mg) was added in portions. After the addition, the reaction mixture was stirred at room temperature for 12 hours. The pyridine was then removed *in vacuo*. The residue was taken up in methylene chloride/diethyl ether (1/1,

v/v, 100 ml). The mixture was washed with dilute brine (3 x 20 ml), dried over MgSO₄, and concentrated to give a liquid residue. The crude product was purified by column chromatography with ethyl acetate/hexane (4/6, v/v) as eluent to give the clean product as a colorless oil (25 g) in 74% yield.

Analogous reactions will append a carboxyamido group.



REACTION 10

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Conformational Analysis - EXAMPLES:

The following Examples are included herein solely to provide a more complete understanding of the invention. The Examples do not limit the scope of the invention disclosed and claimed herein in any fashion.

Example 1: Amide Proton Exchange in *trans*-ACHC Dimer and Hexamer:

Amide proton exchange is one of the most powerful methods for assessing conformational stability of peptides and proteins; adoption of a stable intramolecularly hydrogen-bonded conformation leads to diminution of the rate of exchange. NH/ND exchange behavior of the *trans*-ACHC hexamer relative to the corresponding dimer (which is too small to form a favorable internal hydrogen bond) shows that the hexamer adopts a very stable intramolecularly hydrogen-bonded folding pattern in methanol solution.

To ensure a direct comparison, this Example was conducted with solutions containing 2 mM of the *trans*-ACHC dimer and 2 mM of the *trans*-ACHC hexamer. The ^1H NMR results are shown in Fig. 3. Upon dissolution of the 1:1 dimer:hexamer mixture in CD_3OD , the amide proton and the urethane proton of the dimer (marked with asterisks) are completely exchanged within 6 min, according to ^1H NMR (Fig. 3). In contrast, three of the six amide protons of the *trans*-ACHC hexamer show strong resonances at this point.

One of these protected protons exchanges within a ca. 20 h, but the other two require > 2 days for complete exchange. Thus, two of the amide protons of hexamer display > 100-fold protection from NH/ND exchange with CD_3OD , which indicates remarkable conformational stability for this six-residue foldamer in a hydrogen-bonding solvent. The two most protected protons of the hexamer are believed to be the amide groups of

residues 2 and 3 (numbering from the N-terminus), although Applicants do not wish to be limited to this interpretation. The amide protons of residues 5 and 6 should exchange rapidly because they cannot be involved in 14-helical hydrogen bonds. The protons of residues 1 and 4 occur at the ends of the 14-helix in the hexamer crystal. The ends of α -helices in short α -peptides are "frayed" in solution, and similar fraying in the *trans*-ACHC hexamer would presumably enhance the NH/ND exchange rate. This conclusion is supported by the observation that only one of the NH resonances of the corresponding tetramer can be detected by ^1H NMR within a few minutes of dissolution in CD_3OD , and this proton exchanges completely in less than an hour. Adoption of a stable folding pattern in solution requires the intrinsic rigidity of the *trans*-ACHC residue; dissolution of an analogous β -alanine hexamer in CD_3OD causes all NH groups to exchange within 6 min. This Example shows that *trans* β -peptide oligomers constructed from an appropriately rigidified residue are highly predisposed to form a specific helix.

Example 2: Circular Dichroism and NOE's in *trans*-ACPC

As noted above, computational comparisons involving alternative cycloalkane-based β -amino acids and alternative β -peptide helices suggested that the *trans*-ACHC/14-helix combination would generate a stable β -peptide secondary structure. Using the same technique, the *trans*-ACPC/12-helix combination was predicted to be almost as favorable. This latter prediction is intriguing because there is no precedent for the 12-helix in the contradictory literature on polymers constructed from optically active β -amino acids. Among these polymers, poly(α -isobutyl-L-aspartate) has been particularly intensively studied, and proposed secondary structures include 14-, 16-, 18- and 20-helix, as well as sheet. Since the computational predictions regarding the *trans*-ACHC/14-helix relationship

described above proved to be correct, the *trans*-ACPC/12-helix prediction was then explored.

Optically active *trans*-ACPC was prepared using the protocols described above, and β -peptides were generated via standard coupling methods. A *trans*-ACPC octamer displays the predicted 12-helical conformation in the solid state; all six of the possible 12-membered ring hydrogen bonds are formed. A *trans*-ACPC hexamer also displays the predicted 12-helical conformation in the solid state, with all four of the possible 12-membered ring hydrogen bonds formed. In both cases, the regular helix frays at the C-terminus, perhaps because the C-terminal ester group cannot serve as a hydrogen bond donor.

Circular dichroism data for *trans*-ACPC hexamer in CH₃OH (Fig. 4) indicates the adoption of a distinctive secondary structure. The main graph in Fig. 4 depicts two virtually superimposable CD plots: one at a hexamer concentration of 2.0 mM, the other at hexamer concentration of 0.1 mM. Data were obtained on a Jasco J-715 instrument at 20°C using a 1 mm pathlength. The inset graph shows the CD data at 0.1 mM and 0.02 mM using a 5 mm pathlength. The 14-helical conformation in β -peptides composed of acyclic residues has a far-UV CD signature comprising a maximum at ca. 197 nm, a zero crossing at ca. 207 nm, and minimum at ca. 215 nm. In contrast, the CD signature for the *trans*-ACPC hexamer is clearly different: maximum at ca. 204 nm, zero crossing at ca. 214 nm, and minimum at ca. 221 nm. Since the CD signature of *trans*-ACPC hexamer in CH₃OH does not vary significantly between 2.0 mM and 0.02 mM, it is unlikely that aggregation occurs under these conditions.

Two-dimensional ¹H NMR data obtained for the *trans*-ACPC hexamer in pyridine-d₅ and in CD₃OH indicate that the 12-helix is highly populated in these solvents. Resonances of all NH groups, all protons at C _{β} of each *trans*-ACPC residue, and nearly all protons at C _{α} of each residue

were resolved in pyridine-d₅, and could be assigned via a combination of TOCSY and ROESY data. The N-terminal NH (residue 1) could be identified because it was the only one of the six amidic protons that did not show an NOE to C_αH of another residue (this NH also showed an NOE to the Boc methyl groups). The C-terminal residue could be identified because it had the only C_αH that did not show an NOE to an NH of another residue. Assignment of these terminal resonances allowed us to "walk through" the remaining backbone resonances by virtue of short-range C_αH_i → NH_{i+1} NOEs.

The secondary structure of the *trans*-ACPC hexamer in pyridine-d₅ is defined by the long-range NOEs summarized in Table 1, below. C_βH_i → NH_{i+2} and C_βH_i → C_αH_{i+2} NOEs are expected for the 12-helix. All four possible C_βH_i → NH_{i+2} NOEs were observed for the ACPC hexamer, as were two of the four C_αH_i → C_αH_{i+2} NOEs; NOEs consistent with the other two C_βH_i → C_αH_{i+2} interactions were observed but could not be unambiguously assigned because of overlap of the C_αH resonances of residues 3 and 4. An NOE between NH of residue 3 and the Boc methyl groups provided further evidence for 12-helical folding. In CD₃OH, NOEs consistent with all of the long range NOEs detected in pyridine-d₅ were observed, and there did not appear to be any additional NOEs in CD₃OH. Interpretation of the CD₃OH data was less definitive, however, because of greater overlap among proton resonances (especially for C_βH of the *trans*-ACPC residues). The pattern of NOEs in CD₃OH was identical for 25 mM and 2.5 mM samples of the *trans*-ACPC hexamer; chemical shifts and line widths were also invariant between these two concentrations, suggesting that aggregation does not occur under these conditions.

Table 1 Inter-residue NOEs of hexamer 2 in pyridine-d₅

Residue	H-atom	Residue	H-atom	NOE*
1	C _α H	2	NH	Strong
1	C _β H	2	NH	Weak
1	C _β H	3	NH	Medium
1	C _β H	3	C _α H	Medium†
1	CH ₃ (Boc)	3	NH	Strong
1	C _β H	4	NH	Weak
2	C _α H	3	NH	Strong
2	C _β H	4	NH	Medium
2	C _β H	4	C _α H	Medium†
3	C _α H	4	NH	Strong
3	C _β H	5	NH	Medium
3	C _β H	5	C _α H	Medium
4	C _α H	5	NH	Strong
4	C _β H	6	NH	Medium
4	C _β H	6	C _α H	Weak
5	C _α H	6	NH	Strong
5	C _β H	6	NH	Weak

* Strong, 2.3 Å; medium, 3.0 Å; weak, 4.0 Å.

† NOE present, but overlap of C_αH of residues 3 and 4 prevents definite assignment.

5 NOE-restrained molecular dynamics simulations of the *trans*-ACPC hexamer generated 10 low-energy conformations. Superposition of these conformers shows a high degree of order (RMSD of backbone atoms <0.2 Å), with fraying at the C-terminus). The conformer from this set that is closest to the average agrees quite well with the crystal structure of the hexamer, although there is variation at the C-terminus and in individual cyclopentane ring conformations.

10 Fig. 5 shows CD data for the dimer, trimer, tetramer, and hexamer of *trans*-ACPC in methanol. A comparison between the dimer and the hexamer indicates the profound change in secondary structure which takes place as the peptide chain increases in length. The dimer is essentially unstructured. However, the tetramer clearly displays a CD curve indicative of 12-helical secondary structure.

15 This Example shows that short β-peptides of *trans*-ACPC have a high propensity to adopt the 12-helical folding pattern. In combination with the 14-helix formation by short oligomers of *trans*-ACHC, the present results indicate that β-peptide secondary structure can be profoundly and rationally altered by manipulating torsional preferences about the C_α-C_β bonds of individual residues.

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25 **Example 3: Amide Proton Exchange in Amino-Substituted *trans*-ACHA/*trans* ACHA Dimers and Hexamers:**

In this Example, amino-substituted-*trans*-ACHA (i.e., ACHA containing an exocyclic amino substituent) was synthesized according to Reaction 3, above. The amino-substituted-*trans*-ACHA was then coupled with unsubstituted *trans*-ACHA as shown in Reaction 7 to yield β-peptides wherein the residues alternate between unsubstituted-*trans*-ACHA and amino-substituted-*trans*-ACHA. These molecules were synthesized because it was anticipated that the amino group would be protonated in water and

that the resulting positive charge would render these β -peptides water-soluble. They are indeed water-soluble.

The amide exchange of the dimer and the hexamer were then compared in the same fashion as described in Example 1 in order to probe for 14-helix formation in water. Fig. 6 depicts the two-dimensional ^1H NMR data obtained for the alternating unsubstituted-*trans*-ACHA/amino-substituted-*trans*-ACHA hexamer in D_2O , 100 mM deuterioacetate buffer, pD 3.9. Hydrogen/deuterium exchange can be examined at five of the six backbone NH groups in this acidic D_2O solution. The spectra were taken at room temperature. Five NH peaks are observed (marked with asterisks) in the 8 minute plot. Each peak disappears at a different rate over the course of two days as the NH groups become ND groups. The protons slowest to exchange are those hydrogen bonded and buried in a folded secondary conformation.

As shown in Fig. 7, the rate of amide proton exchange in the dimer had a k_{obs} of $6.6 \times 10^{-4}/\text{sec}$. In contrast, the slowest amide proton exchange in the hexamer had a k_{obs} of $1 \times 10^{-4}/\text{sec}$, more than 6-fold slower (protection factor = 6.6). In other words, the slowest exchanging NH of the hexamer takes 6.6 times longer to exchange than the NH of the dimer (which is too small to adopt a folded conformation). This Example shows that there is substantial peptide folding of the alternating unsubstituted-*trans*-ACHA/amino-substituted-*trans*-ACHA hexamer in aqueous solution. The data strongly suggest that the hexamer is forming a 14-helix.

Example 4: Comparison of CD Data from Amino-Substituted *trans*-ACHA/*trans*-ACHA Hexamers and *trans*-ACHC:

In this Example, the CD data from the alternating hexamer described in Example 3 was compared with a hexamer of unsubstituted *trans*-ACHC. The *trans*-ACHC hexamer adopts a 14-helical conformation in methanol

solution. Therefore, the CD plot for *trans*-AHC should be representational of the 14-helix structure and can serve as a means of comparison for other peptides. Fig. 8 compares the CD data of *trans*-AHC hexamer in methanol with the CD data of the alternating unsubstituted-*trans*-AHC/amino-substituted-*trans*-AHC described in Example 3. The similarity of the two plots provides strong evidence that the alternating hexamer adopts a 14-helical conformation in aqueous solution. In contrast, conventional peptides made from α -amino acids never show evidence of α -helicity where there are fewer than 10 residues.

Examples 3 and 4 in combination show that in addition to the substantial peptide folding indicated by the slow amide proton exchange rate of the alternating hexamer, the CD data strongly indicates that the alternating hexamer adopts a 14-helix secondary structure in aqueous solution.

Example 5: CD Data of β -Peptides Containing Alternating *trans*-ACPA Residues and 3-Amino-4-Carboxy-Pyrrolidinyl Residues

In this Example, a β -amino acid containing a 3-amino-4-carboxy-pyrrolidinyl residue was synthesized according to Reaction 5, and coupled into a series of peptides with alternating *trans*-ACPA residues using conventional coupling methods (Reaction 7). CD data for the tetramer, hexamer, and octamer in this series were then gathered. The results, in methanol, are shown in Fig. 9. Note the distinct and increasing intensity of the characteristic maximum at about 205 nm and minimum at about 221 nm as the chain length increases.

Fig. 10 shows another plot of CD data, in this instance using water as the solvent. Again, the maximum and minimum characteristic peaks increase in intensity with increasing chain length.

Fig. 11 is a direct comparison of the CD data in water versus the CD data in methanol for the alternating 4-pyrrolidinyl/*trans*-ACPA octamer. These data indicate that the 12-helix formation is only slightly less stable in water than it is in methanol.

Taken together, the CD data presented in this Example strongly indicate that the pyrrolidinyl β -peptides assume a 12-helix conformation in both methanol and aqueous solutions.

Example 6: CD Data of Octamer Containing Alternating *trans*-ACPA Residues and 3-Amino-2-Carboxy-Pyrrolidinyl residues.

In this Example, a β -amino acid containing a 3-amino-2-carboxy-pyrrolidinyl residue was synthesized according to Reaction 4, and coupled into a peptide with alternating *trans*-ACPA residues using conventional coupling methods (Reaction 7). CD data for the octamer of this peptide was then gathered. The results, in aqueous solution, are shown in Fig. 12. This β -peptide clearly adopts the 12-helix conformation in water as evidenced by the characteristic maximum at about 205 nm and the characteristic minimum at about 221 nm.

This Example shows that the nitrogen heteroatom introduced in the pyrrolidinyl moiety can be located in different postions along the heterocyclic ring without adversely affecting the formation of the 12-helical structure in solution.

Example 7: Comparison of Secondary Structure in Amino-Substituted-*trans*-ACHC and β -Peptides Containing Aliphatic-Substituted Residues

In this Example, the CD spectrum of a β -peptide containing alternating residues of *trans*-ACHA and amino-substituted-*trans*-ACHA was compared to the CD spectrum of a "mixed" β -peptide comprising alternating

residues of *trans*-ACHA and an acyclic β -amino acid bearing an aminopropyl substituent on the β -carbon of the backbone. The acyclic β -amino acid was synthesized and coupled to the *trans*-ACHA residue as detailed in Reaction 9, described above.

The CD data are presented in Fig. 13. While the removal of 3 cyclohexyl units clearly diminishes the extent of helix formation, the extent of helix formation in the mixed β -peptide is still significant. The data presented here indicate that β -peptides which include acyclic residues along with ring-constrained residues will adopt moderately stable secondary structures in solution.

Example 8: Infrared Analysis of Reverse Turn Using Linked Nipecotic Acid Moieties

In this Example, two nipecotic acid residues were linked to each other to act as a reverse turn moiety. This was done using Reaction 6. Fig. 14A shows the IR spectrum for the diastereomer in which the two nipecotic acid residues have the same absolute configuration and Fig. 14B shows the IR spectrum for the diastereomer in which the two nipecotic acid residues have opposite absolute configuration. Both samples were taken in dilute solution (to minimize intermolecular hydrogen bonding) with solvent subtraction. As is clear from the diastereomer shown in Fig. 14A, there is little intramolecular hydrogen bonding as evidenced by the large peak at 3454 cm^{-1} which is due to N-H units not involved in hydrogen bonding. This was as predicted from computer modeling studies.

In contrast, the spectrum shown in Fig. 14B for the heterochiral diastereomer exhibits a very large peak at 3350 cm^{-1} , indicative of hydrogen-bonded N-H groups.

This Example shows that synthetic reverse turn moieties can be constructed from two nipecotic β -amino acid residues having opposite configuration.

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Example 9: X-ray Crystallography of Synthetic Reverse Turn

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Compound 1 was synthesized as described above. Crystals of compound 1 suitable for X-ray analysis were obtained by vapor diffusion (over 2 weeks) of n-heptane into a solution of the sample in ethyl acetate. The data were collected on a Siemens P4/CCD diffractometer running software provided by the manufacturer. The ball and stick schematic of the crystal structure in the solid state is presented in Fig. 16. All hydrogens except those bonded to nitrogen have been removed for clarity. Hydrogen bonds are shown in dotted lines.

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Combinatorial Chemistry:

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The defined conformation conferred by the β -polypeptides described herein makes these polyamide compounds highly useful for constructing large libraries of potentially useful compounds via combinatorial chemistry. Combinatorial exploration of functionalized oligomers of, for instance, *trans*-ACHC, *trans*-ACPC, or β -peptides wherein the α and β carbons are part of a cycloalkenyl ring or a heterocyclic ring such a pyrrolidinyl or piperidinyl moiety, or "mixed" β -peptides containing acyclic residues in addition to cyclic residues, has a potential yield of literally millions of novel polypeptide molecules, all of which display a well-defined helical or sheet secondary structure.

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Of particular note here is that the equatorial positions of the cyclohexyl β -peptides can be substituted with virtually any substituent, including very large substituents, without disrupting the helical secondary

structure. At least in helical structures, this is because any equatorial substituent extends essentially perpendicular from the axis of rotation of the helix, thereby leaving the hydrogen bonds of the helix undisturbed.

The amino acids which comprise the finished peptides can be functionalized prior to being incorporated into a polypeptide, or an unfunctionalized polypeptide can be constructed and then the entire oligomer functionalized. Neither method is preferred over the other as they are complementary depending upon the types of compounds which are desired.

Combinatorial libraries utilizing the present compounds may be constructed using any means now known to the art or developed in the future. The preferred methods, however, are the "split and pool" method using solid-phase polypeptide synthesis on inert solid substrates and parallel synthesis, also referred to as multipin synthesis.

The "split and pool" concept is based on the fact that combinatorial bead libraries contain single beads which display only one type of compound, although there may be up to 10^{13} copies of the same compound on a single 100 μm diameter bead. The process proceeds as follows, utilizing standard solid-phase peptide synthesis as described above:

Several suitable solid substrates are available commercially. The substrates are generally small diameter beads, *e.g.* about 100 μm , formed from inert polymeric materials such as polyoxyethylene-grafted polystyrene or polydimethylacrylamide. An illustrative substrate, marketed under the trademark "ARGOGEL" is available from Argonaut Technologies, Washington, D.C.

Referring now to Fig. 15, which is a schematic depicting the split and pool method, a plurality of inert substrates are divided into two or more groups and then a first set of subunits is covalently linked to the inert support. As depicted in Fig. 15, the initial plurality of substrates is divided into three subgroups. The appearance of the three groups of beads after the

first round of coupling is shown at I of Fig. 15. The three groups of beads
are then pooled together to randomize the beads. The beads are then again
split into a number of subgroups. Another round of coupling then takes
place wherein a second subunit is bonded to the first subunit already present
on each bead. The process is then repeated (theoretically *ad infinitum*) until
the desired chain length is attained.

The split and pool process is highly flexible and has the capability of
generating literally millions of different compounds which, in certain
applications, can be assayed for activity while still attached to the inert
substrate.

A critical aspect of the split and pool methodology is that each
reaction be driven to completion prior to initiating a subsequent round of
coupling. So long as each coupling reaction is driven to completion, each
substrate bead will only display a single compound. Because the rate of
reaction will differ from bead to bead as the library construction progresses,
the beads can be monitored using conventional dyes to ensure that coupling
is completed prior to initiating another round of synthesis. The presence of
only a single compound per bead comes about because each individual bead
encounters only one amino acid at each coupling cycle. So long as the
coupling cycle is driven to completion, all available coupling sites on each
bead will be reacted during each cycle and therefore only one type of
peptide will be displayed on each bead.

The resulting combinatorial library is comprised of a plurality of
inert substrates, each having covalently linked thereto a different β -
polypeptide. The polypeptides can be screened for activity while still
attached to the inert support, if so desired and feasible for the activity being
investigated. Beads which display the desired activity are then isolated and
the polypeptide contained thereon characterized via conventional peptide
chemistry, such as the Edman degradation. Where a solution-phase assay

is to be used to screen the library, the polypeptides are cleaved from the solid substrate and tested in solution.

As applied in the present invention, one or more of the subunits coupled to the inert substrate are selected from the β -amino acids described herein. In this fashion, large libraries of β -polypeptides can be assembled, all of compounds contained therein which display predictable secondary structure.

An alternative approach to generating combinatorial libraries uses parallel synthesis. In this approach, a known set of first subunits is covalently linked to a known location on a inert substrate, one subunit type to each location. The substrate may be a series of spots on a suitable divisible substrate such as filter paper or cotton. A substrate commonly used is an array of pins, each pin being manufactured from a suitable resin, described above.

After the initial round of coupling, each pin of the array bears a first subunit covalently linked thereto. The array is then reacted with a known set of second subunits, generally different from the first, followed by reactions with a third set of subunits, and so on. During each reiteration, each individual pin (or location) is coupled with a incoming subunit selected from a distinct set of subunits, with the order of the subunits being recorded at each step. The final result is an array of polypeptides, with a different polypeptide bonded to each solid substrate. Because the ordering of the subunits is recorded, the identity of the primary sequence of the polypeptide at any given location on the substrate (*i.e.*, any given pin) is known. As in the split and pool method, each coupling reaction must be driven to completion in order to ensure that each location on the substrate contains only a single type of polypeptide.

Large Molecule Interactions:

Another use for the present compounds is as molecular probes to investigate the interactions between biological macromolecules to identify antagonists, agonists, and inhibitors of selected biological reactions. As noted above, many biological reactions take place between very large macromolecules. The surface areas in which these reactions take place are thought by many to be far too large to be disrupted, altered, or mimicked by a small molecule. Until the present invention, it has been difficult, if not impossible, to manufacture molecular probes of modest size that display a well-defined conformation. Because the compounds described herein assume a highly predictable helical or sheet conformation, even when functionalized, they find use as reagents to probe the interaction between large biomolecules.

Employing the combinatorial methods described herein greatly expands the medicinal application of the compounds as vast libraries of compounds can be screened for specific activities, such as inhibitory and antagonist activity in a selected biological reaction.

It is understood that the invention is not confined to the particular reagents, reactions, and methodologies described above, but embraces all modified and equivalent forms thereof as come within the scope of the following claims.